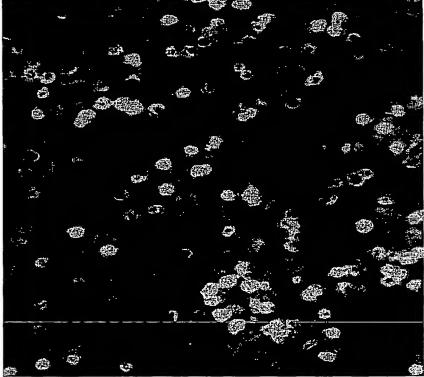
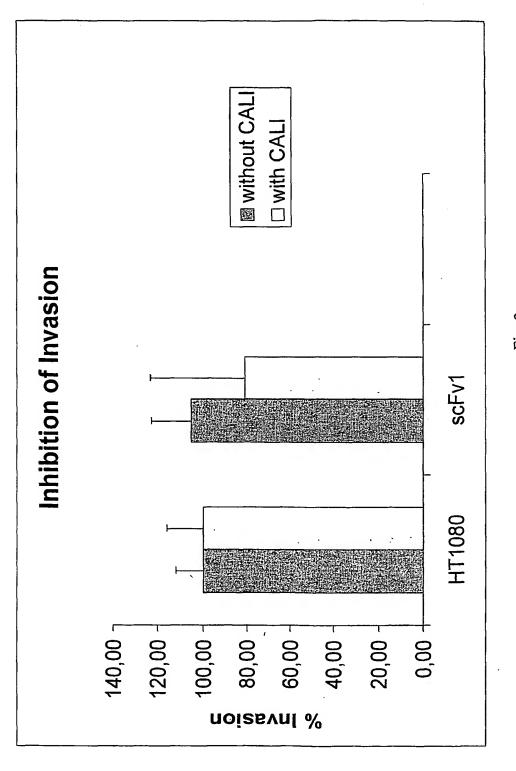


Invasion of Hs-27 control cells

Fig. 1



Invasion of HT1080 cells



F1g. 2

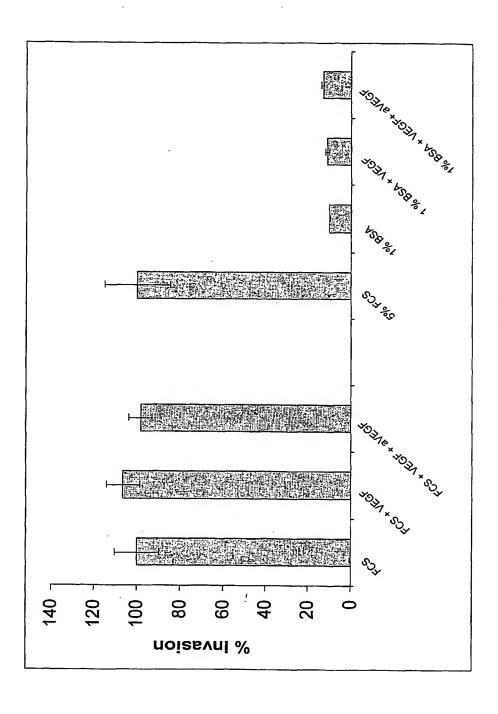


Fig. 2a

10/539402

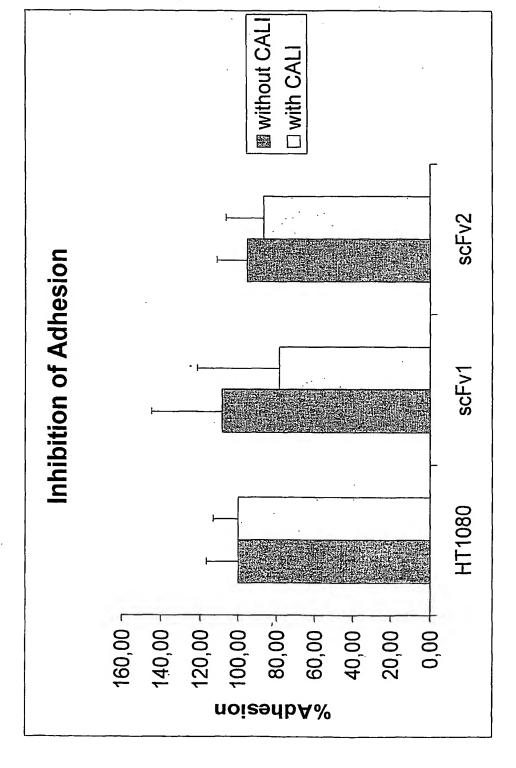


Fig. 3

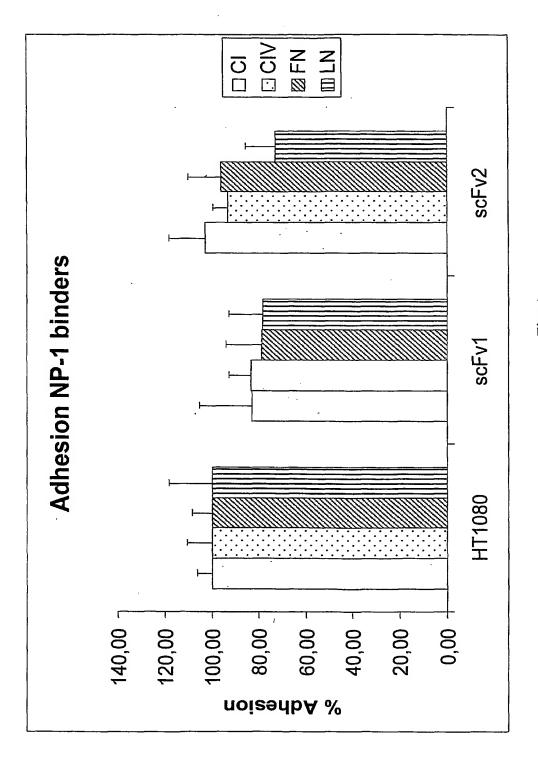
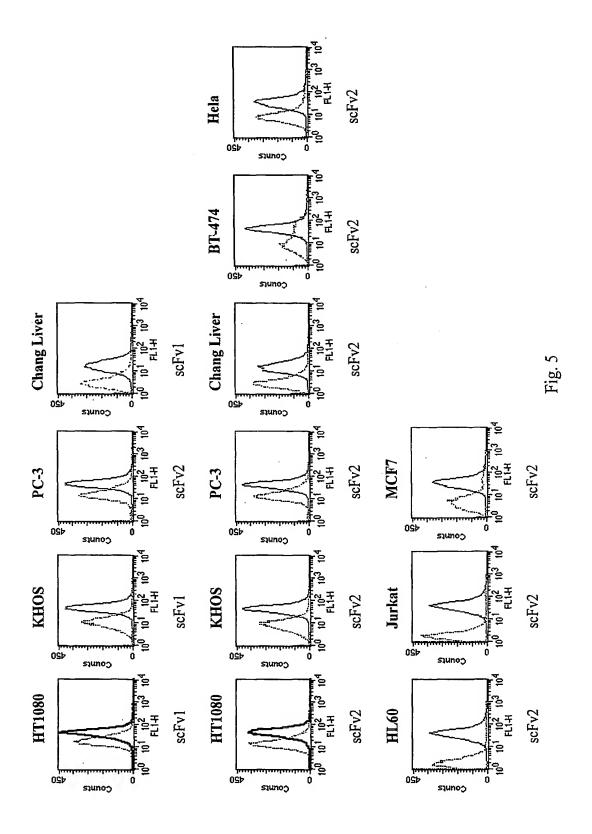


Fig. 4



PCT/EP2003/014756

~ 130 kDa = Neuropilin

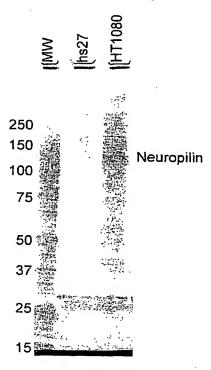


Fig. 6

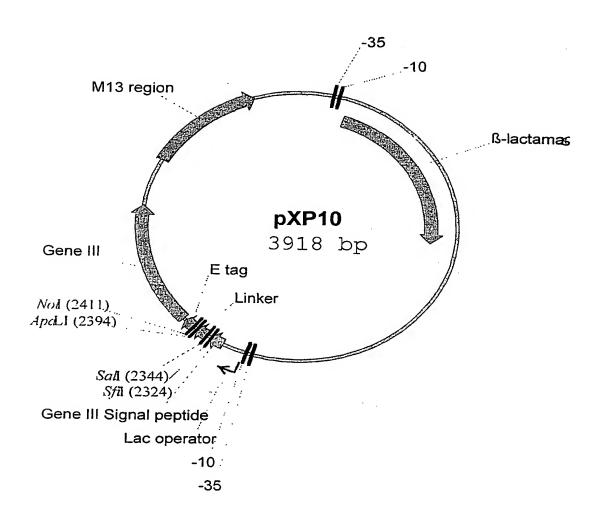


Fig. 7a

• |

| Nucleo | tide Sequence | e nVD10    |            |             |            |
|--------|---------------|------------|------------|-------------|------------|
| 1      | age Seducite  | s hvr in   |            |             |            |
| 1      | GACGAAAGGG    | CCTCGTGATA | CGCCTATTTT | TATAGGTTAA  | TGTCATGATA |
|        | CTGCTTTCCC    | GGAGCACTAT | GCGGATAAAA | ATATCCAATT  | ACAGTACTAT |
| 51     | ATAATGGTTT    | CTTAGACGTC | AGGTGGCACT | TTTCGGGGAA  | ATGTGCGCGG |
|        | TATTACCAAA    | GAATCTGCAG | TCCACCGTGA | AAAGCCCCTT  | TACACGCGCC |
| 101    | AACCCCTATT    | TGTTTATTTT | TCTAAATACA | TTCAAATATG  | TATCCGCTCA |
|        | TTGGGGATAA    | ACAAATAAAA | AGATTTATGT | AAGTTTATAC  | ATAGGCGAGT |
| 151    | TGAGACAATA    | ACCCTGATAA | ATGCTTCAAT | AATATTGAAA  | AAGGAAGAGT |
|        | ACTCTGTTAT    | TGGGACTATT | TACGAAGTTA | TTATAACTTT  | TTCCTTCTCA |
| 201    | ATGAGTATTC    | AACATTTCCG | TGTCGCCCTT | ATTCCCTTTT  | TTGCGGCATT |
|        | TACTCATAAG    | TTGTAAAGGC | ACAGCGGGAA | TAAGGGAAAA  | AACGCCGTAA |
| 251    | TTGCCTTCCT    | GTTTTTGCTC | ACCCAGAAAC | GCTGGTGAAA  | GTAAAAGATG |
|        |               | CAAAAACGAG | TEGETCTTTE | CCACCACTT   | CATTTTCTAC |
| 301    | CTGAAGATCA    | GTTGGGTGCT | CCACTCCCTT | ACATCGAACT  | CATTITUTAL |
|        | GACTTCTAGT    | CAACCCACGA | CCTCACCCAA | TCTICGTTCI  | COMPORTO   |
| 351    | AGCGGTAAGA    | TCCTTGAGAG | TOTORCCCAA | GAAGAACGTT  |            |
|        |               | AGGAACTCTC | AAAACCCCCC | COMMONACGIT | TTCCAATGAT |
| 401    | GAGCACTTTT    | AAAGTTCTGC | MAMAGCGGGG | CITCITGCAA  |            |
|        |               |            | ATTOTOGCGC | GGTATTATCC  | CGTATTGACG |
| 451    | CCCCCCAACA    | TTTCAAGACG | ATACACCGCG | CCATAATAGG  | GCATAACTGC |
| 401    | CCCCCCTTCT    | GCAACTCGGT | CGCCGCATAC | ACTATTCTCA  | GAATGACTTG |
| 501    | COUCACUACO    | CGTTGAGCCA | GCGGCGTATG | TGATAAGAGT  | CTTACTGAAC |
| 301    | GIIGAGIACI    | CACCAGTCAC | AGAAAAGCAT | CTTACGGATG  | GCATGACAGT |
| 551    | AACACAATGA    | GTGGTCAGTG | TCTTTTCGTA | GAATGCCTAC  | CGTACTGTCA |
| 331    | AAGAGAATTA    | TGCAGTGCTG | CCATAACCAT | GAGTGATAAC  |            |
| 601    | TTCTCTTAAT    | ACGTCACGAC |            |             |            |
| 601    | ACTTACTTCT    | GACAACGATC | GGAGGACCGA |             | CGCTTTTTTG |
| 651    | TGAATGAAGA    | CTGTTGCTAG | CCTCCTGGCT | TCCTCGATTG  | GCGAAAAAAC |
| 651    | CACAACATGG    | GGGATCATGT | AACTCGCCTT | GATCGTTGGG  | AACCGGAGCT |
| 701    | GTGTTGTACC    | CCCTAGTACA | TTGAGCGGAA | CTAGCAACCC  | TTGGCCTCGA |
| 701    | GAATGAAGCC    | ATACCAAACG | ACGAGCGTGA |             |            |
| 25.    | CTTACTTCGG    | TATGGTTTGC | TGCTCGCACT | GTGGTGCTAC  | GGACATCGTT |
| 751    | TGGCAACAAC    | GTTGCGCAAA |            |             |            |
|        |               | CAACGCGTTT | GATAATTGAC | CGCTTGATGA  | ATGAGATCGA |
| 801    | TCCCGGCAAC    | AATTAATAGA | CTGGATGGAG | GCGGATAAAG  | TTGCAGGACC |
|        | AGGGCCGTTG    |            | GACCTACCTC | CGCCTATTTC  | AACGTCCTGG |
| 851    | ACTTCTGCGC    | TCGGCCCTTC | CGGCTGGCTG | GTTTATTGCT  | GATAAATCTG |
|        | TGAAGACGCG    | AGCCGGGAAG | GCCGACCGAC | CAAATAACGA  | CTATTTAGAC |
| 901    |               | GCGTGGGTCT |            |             | GGGGCCAGAT |
|        | CTCGGCCACT    |            | GCGCCATAGT | AACGTCGTGA  | CCCCGGTCTA |
| 951    | GGTAAGCCCT    | CCCGTATCGT | AGTTATCTAC | ACGACGGGGA  | GTCAGGCAAC |
|        | CCATTCGGGA    | GGGCATAGCA | TCAATAGATG | TGCTGCCCCT  | CAGTCCGTTG |
| 1001   | TATGGATGAA    | CGAAATAGAC | AGATCGCTGA | GATAGGTGCC  | TCACTGATTA |
|        | ATACCTACTT    |            | TCTAGCGACT | CTATCCACGG  | AGTGACTAAT |
| 1051   | AGCATTGGTA    | ACTGTCAGAC | CAAGTTTACT | CATATATACT  | TTAGATTGAT |
|        | TCGTAACCAT    | TGACAGTCTG | GTTCAAATGA | GTATATATGA  | AATCTAACTA |
| 1101   | TTAAAACTTC    | ATTTTTAATT | TAAAAGGATC | TAGGTGAAGA  | TCCTTTTTGA |
|        | AATTTTGAAG    | TAAAAATTAA | ATTTTCCTAG | ATCCACTTCT  | AGGAAAAACT |
| 1151   | TAATCTCATG    | ACCAAAATCC | CTTAACGTGA | GTTTTCGTTC  | CACTGAGCGT |
|        | ATTAGAGTAC    | TGGTTTTAGG | GAATTGCACT | CAAAAGCAAG  | GTGACTCGCA |
| 1201   | CAGACCCCGT    | AGAAAAGATC | AAAGGATCTT | CTTGAGATCC  | ጥጥጥጥጥጥርጥር  |
|        | GTCTGGGGCA    | TCTTTTCTAG | TTTCCTAGAA | GAACTCTAGG  | AAAAAAAGAC |
| 1251   | CGCGTAATCT    | GCTGCTTGCA | AACAAAAAA  | CCACCGCTAC  | CAGCGGTGGT |
|        | GCGCATTAGA    | CGACGAACGT | TTGTTTTTTT | GGTGGCGATG  | GTCGCCACCA |
| 1301   | TTGTTTGCCG    | GATCAAGAGC | TACCAACTCT | TTTTCCGAAG  | GTAACTGGCT |
|        | AACAAACGGC    | CTAGTTCTCG | ATGGTTGAGA | AAAAGGCTTC  | CATTGACCGA |
| 1351   | TCAGCAGAGC    | GCAGATACCA | AATACTGTCC | TTCTAGTGTA  | GCCGTAGTTA |
|        |               |            |            |             |            |

|                |            | G CGTCTATGGT             |             | AAGATCACAT      | CGGCATCAAT               |
|----------------|------------|--------------------------|-------------|-----------------|--------------------------|
| 1401           |            | TCAAGAACTC               |             | CCTACATACC      |                          |
| <del>-</del> - |            | AGTTCTTGAG               |             |                 | AGCGAGACGA               |
| 1451           | AATCCTGTTA | CCAGTGGCTG               |             | CGATAAGTCG      | TGTCTTACCG               |
|                | TTAGGACAA1 |                          | GACGGTCACC  | GCTATTCAGC      | ACAGAATGGC               |
| 1501           | GGTTGGACTC | AAGACGATAG               | TTACCGGATA  | AGGCGCAGCG      | GTCGGGCTGA               |
|                | CCAACCTGAG |                          | AATGGCCTAT  | TCCGCGTCGC      | CAGCCCGACT               |
| 1551           | ACGGGGGGTI | CGTGCATACA               | GCCCAGCTTG  |                 | CCTACACCGA               |
|                |            | GCACGTATGT               |             | CTCGCTTGCT      | GGATGTGGCT               |
| 1601           | ACTGAGATAC | CTACAGCGTG               | AGCTATGAGA  | AAGCGCCACG      | CTTCCCGAAG               |
|                | TGACTCTATG | GATGTCGCAC               | TCGATACTCT  |                 |                          |
| 1651           | GGAGAAAGGC | GGACAGGTAT               | CCGGTAAGCG  |                 | AACAGGAGAG               |
|                | CCTCTTTCCG | CCTGTCCATA               | GGCCATTCGC  |                 |                          |
| 1701           | CGCACGAGGG | AGCTTCCAGG               |             |                 |                          |
|                | GCGTGCTCCC |                          |             |                 | TATCAGGACA               |
| 1751           | CGGGTTTCGC |                          | TTGAGCGTCG  | ATTTTTGTGA      | TGCTCGTCAG               |
|                | GCCCAAAGCG | GTGGAGACTG               | AACTCGCAGC  | TAAAAACACT      |                          |
| 1801           | GGGGGCGGAG | CCTATGGAAA               | AACGCCAGCA  | ACCCCCCCTT      | TTTACGGTTC               |
|                |            | GGATACCTTT               | TTGCGGTCGT  |                 | AAATGCCAAG               |
| 1851           | CTGGCCTTTT |                          |             |                 | CGTTATCCCC               |
|                |            | CGACCGGAAA               | ACCACTCATAC | AVCAVACCAC      |                          |
| 1901           | TGATTCTGTG |                          | TTACCGCCTT  |                 | GCAATAGGGG<br>GATACCGCTC |
|                | ACTAAGACAC |                          |             | J CTC J CTC C Z | CTATGGCGAG               |
| 1951           |            | AACGACCGAG               | CCCACCCACM  | CACTCACTCGA     | CTATGGCGAG               |
|                | CGGCGTCGGC |                          |             |                 | GGAAGCGGAA               |
| 2001           | •          | TACGCAAACC               | GCGTCGCTCA  |                 | CCTTCGCCTT               |
| 2001           | CTCGCGGGTT |                          |             |                 |                          |
| 2051           |            | CACGACAGGT               | CGGAGAGGGG  | CGCGCAACCG      |                          |
| 2001           | TACGTCGACC |                          |             | GAAAGCGGGC      | AGTGAGCGCA               |
| 2101           |            |                          |             | CTTTCGCCCG      |                          |
| 2101           | TGCGTTAATT | TGTGAGTTAG               | CTCACTCATT  | AGGCACCCCA      | _                        |
| 2151           |            | ACACTCAATC<br>CGGCTCGTAT | GAGTGAGTAA  | TCCGTGGGGT      | CCGAAATGTG               |
| 2131           |            |                          |             | ATTGTGAGCG      |                          |
| 2201           |            | GCCGAGCATA               |             | TAACACTCGC      | CTATTGTTAA               |
| 2201           |            |                          |             | CGCCAAGCTT      | TGGAGCCTTT               |
| 2251           | AGTGTGTCCT |                          | TGGTACTAAT  | GCGGTTCGAA      |                          |
| 2231           | TTTTTGGAGA |                          | GAAAAAATTA  |                 | TTCCTTTAGT               |
| 2201           | AAAAACCTCT | AAAAGTTGCA               |             |                 | AAGGAAATCA               |
| 2301           | TGTTCCTTTC | TATGCGGCCC               | AGCCGGCCAT  | GGCCCAGGTC      | CAGTCGACAG               |
| 2251           |            | ATACGCCGGG               | TCGGCCGGTA  | CCGGGTCCAG      | GTCAGCTGTC               |
| 2351           | GTGGAGGCGG | TTCAGGCGGA               | GGTGGCTCTG  | GCGGTGGCGG      | AAGTGCACTC               |
| 2403           | CACCTCCGCC | AAGTCCGCCT               | CCACCGAGAC  | CGCCACCGCC      | TTCACGTGAG               |
| 2401           | ATCAAACGGC | GGCCGCAGGT               | GCGCCGGTGC  | CGTATCCGGA      | TCCGCTGGAA               |
|                | TAGTTTGCCG | CCGGCGTCCA               | CGCGGCCACG  |                 | AGGCGACCTT               |
| 2451           | CCGCGTGCCG |                          | CGGCGGCTCT  | GGTGGTGGTT      | CTGGTGGCGG               |
|                | GGCGCACGGC | GTATCCGACC               | GCCGCCGAGA  | CCACCACCAA      | GACCACCGCC               |
| 2501           | CTCTGAGGGT |                          | AGGGTGGCGG  | TTCTGAGGGT      | GGCGGCTCTG               |
|                | GAGACTCCCA | CCGCCGAGAC               | TCCCACCGCC  | AAGACTCCCA      | CCGCCGAGAC               |
| 2551           | AGGGTGGCGG | TTCCGGTGGC               | GGCTCCGGTT  | CCGGTGATTT      | TGATTATGAA               |
|                | TCCCACCGCC | AAGGCCACCG               | CCGAGGCCAA  | GGCCACTAAA      | ACTAATACTT               |
| 2601           | AAAATGGCAA | ACGCTAATAA               | GGGGGCTATG  | ACCGAAAATG      | CCGATGAAAA               |
|                | TTTTACCGTT | TGCGATTATT               | CCCCCGATAC  | TGGCTTTTAC      | GGCTACTTTT               |
| 2651           | CGCGCTACAG | TCTGACGCTA               | AAGGCAAACT  | TGATTCTGTC      | GCTACTGATT               |
|                | GCGCGATGTC | AGACTGCGAT               | TTCCGTTTGA  | ACTAAGACAG      | CGATGACTAA               |
| 2701           | ACGGTGCTGC | TATCGATGGT               | TTCATTGGTG  | ACGTTTCCGG      | CCTTGCTAAT               |
|                | TGCCACGACG | ATAGCTACCA               | AAGTAACCAC  | TGCAAAGGCC      | GGAACGATTA               |
| 2751           | GGTAATGGTG | CTACTGGTGA               | TTTTGCTGGC  | TCTAATTCCC      | AAATGGCTCA               |
|                | CCATTACCAC | GATGACCACT               | AAAACGACCG  | AGATTAAGGG      | TTTACCGAGT               |
|                |            |                          |             |                 |                          |

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| 2801 | AGTCGGTGAC | GGTGATAATT | CACCTTTAAT | GAATAATTTC | CGTCAATATT |
|------|------------|------------|------------|------------|------------|
|      | TCAGCCACTG | CCACTATTAA | GTGGAAATTA | CTTATTAAAG | GCAGTTATAA |
| 2851 | TACCTTCTTT | GCCTCAGTCG | GTTGAATGTC | GCCCTTATGT | CTTTGGCGCT |
|      | ATGGAAGAAA | CGGAGTCAGC | CAACTTACAG | CGGGAATACA | GAAACCGCGA |
| 2901 | GGTAAACCAT | ATGAATTTTC | TATTGATTGT | GACAAAATAA | ACTTATTCCG |
|      | CCATTTGGTA | TACTTAAAAG | ATAACTAACA | CTGTTTTATT | TGAATAAGGC |
| 2951 | TGGTGTCTTT | GCGTTTCTTT | TATATGTTGC | CACCTTTATG | TATGTATTTT |
|      | ACCACAGAAA | CGCAAAGAAA | ATATACAACG | GTGGAAATAC | ATACATAAAA |
| 3001 | CGACGTTTGC | TAACATACTG | CGTAATAAGG | AGTCTTAATA | AGAATTCACT |
|      | GCTGCAAACG | ATTGTATGAC | GCATTATTCC | TCAGAATTAT | TCTTAAGTGA |
| 3051 | GGCCGTCGTT | TTACAACGTC | GTGACTGGGA | AAACCCTGGC | GTTACCCAAC |
|      | CCGGCAGCAA | AATGTTGCAG | CACTGACCCT | TTTGGGACCG | CAATGGGTTG |
| 3101 | TTAATCGCCT | TGCAGCACAT | CCCCCTTTCG | CCAGCTGGCG | TAATAGCGAA |
|      | AATTAGCGGA | ACGTCGTGTA | GGGGGAAAGC | GGTCGACCGC | ATTATCGCTT |
| 3151 | GAGGCCCGCA | CCGATCGCCC | TTCCCAACAG | TTGCGCAGCC | TGAATGGCGA |
|      | CTCCGGGCGT | GGCTAGCGGG | AAGGGTTGTC | AACGCGTCGG | ACTTACCGCT |
| 3201 | ATGGCGCCTG | ATGCGGTATT | TTCTCCTTAC | GCATCTGTGC | GGTATTTCAC |
|      | TACCGCGGAC | TACGCCATAA | AAGAGGAATG | CGTAGACACG | CCATAAAGTG |
| 3251 | ACCGCATACG | TCAAAGCAAC | CATAGTACGC | GCCCTGTAGC | GGCGCATTAA |
|      | TGGCGTATGC | AGTTTCGTTG | GTATCATGCG | CGGGACATCG | CCGCGTAATT |
| 3301 | GCCCGGCGGG | TGTGGTGGTT | ACGCGCAGCG | TGACCGCTAC | ACTTGCCAGC |
|      | CGGGCCGCCC | ACACCACCAA | TGCGCGTCGC | ACTGGCGATG | TGAACGGTCG |
| 3351 | GCCCTAGCCC | CCGCTCCTTT | CGCTTTCTTC | CCTTCCTTTC | TCGCCACGTT |
|      | CGGGATCGGG | GGCGAGGAAA | GCGAAAGAAG | GGAAGGAAAG | AGCGGTGCAA |
| 3401 | CGCCGGCTTT | CCCCGTCAAG | CTCTAAATCG | GGGGCTCCCT | TTAGGGTTCC |
|      | GCGGCCGAAA | GGGGCAGTTC | GAGATTTAGC | CCCCGAGGGA | AATCCCAAGG |
| 3451 | GATTTAGTGC | TTTACGGCAC | CTCGACCCCA | AAAAACTTGA | TTTGGGTGAT |
|      | CTAAATCACG | AAATGCCGTG | GAGCTGGGGT | TTTTTGAACT | AAACCCACTA |
| 3501 | GGTTCACGTA | GTGGGCCATC | GCCCTGATAG | ACGGTTTTTC | GTCCTTTGAC |
|      | CCAAGTGCAT | CACCCGGTAG | CGGGACTATC | TGCCAAAAAG | CAGGAAACTG |
| 3551 | GTTCGAGTCC | ACGTTCTTTA | ATAGTGGACT | CTTGTTCCAA | ACTGGAACAA |
|      | CAAGCTCAGG | TGCAAGAAAT | TATCACCTGA | GAACAAGGTT | TGACCTTGTT |
| 3601 | TACTCAACCC | TATCTCGGGC | TATTCTTTTG | ATTTATAAGG | GATTTTGCCG |
|      | ATGAGTTGGG | ATAGAGCCCG | ATAAGAAAAC | TAAATATTCC | CTAAAACGGC |
| 3651 | ATTTCGGCCT | ATTGGTTAAA | AAATGAGCTG | ATTTAACAAA | AATTTAACGC |
|      | TAAAGCCGGA | TAACCAATTT | TTTACTCGAC | TAAATTGTTT | TTAAATTGCG |
| 3701 | GAATTTTAAC | AAAATATTAA | CGTTTACAAT | TTTATGGTGC | AGTCTCAGTA |
|      | CTTAAAATTG | TTTTATAATT | GCAAATGTTA | AAATACCACG | TCAGAGTCAT |
| 3751 | CAATCTGCTC | TGATGCCGCA | TAGTTAAGCC | AGCCCCGACA | CCCGCCAACA |
|      | GTTAGACGAG | ACTACGGCGT | ATCAATTCGG | TCGGGGCTGT | GGGCGGTTGT |
| 3801 | CCCGCTGACG | CGCCCTGACG | GGCTTGTCTG | CTCCCGGCAT | CCGCTTACAG |
|      | GGGCGACTGC | GCGGGACTGC | CCGAACAGAC | GAGGGCCGTA | GGCGAATGTC |
| 3851 | ACAAGCTGTG | ACCGTCTCCG | GGAGCTGCAT | GTGTCAGAGG | TTTTCACCGT |
|      | TGTTCGACAC | TGGCAGAGGC | CCTCGACGTA | CACAGTCTCC | AAAAGTGGCA |
| 3901 | CATCACCGAA | ACGCGCGA   |            |            |            |
|      | GTAGTGGCTT | TGCGCGCT   |            |            |            |

Fig. 7b

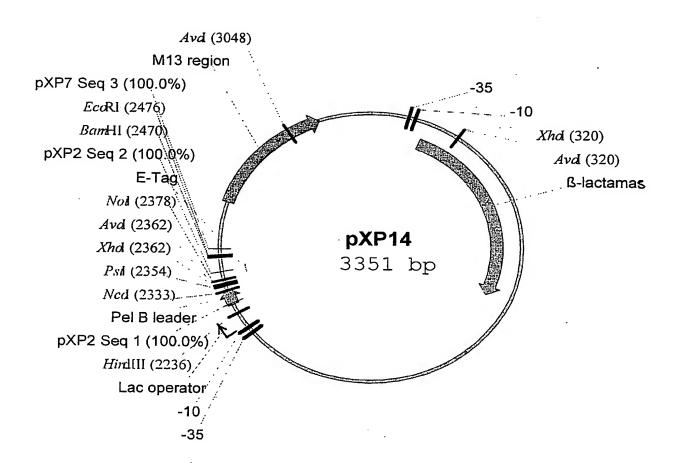


Fig. 8a

#### PCT/EP2003/014756

| Nucleoti | de Sequences 1 | n <b>XP</b> 14 |             |            |            |
|----------|----------------|----------------|-------------|------------|------------|
| 1        |                |                | CCCCM3 mmmm | TATAGGTTAA | mcmcamcama |
| _        | CTGCTTTCCC     |                |             |            |            |
| 51       | ATAATGGTTT     |                |             | ATATCCAATT | ACAGTACTAT |
| 21       | TATTACCAAA     | =              | AGGTGGCACT  |            | ATGTGCGCGG |
| 101      |                |                |             | AAAGCCCCTT | TACACGCGCC |
| 101      | AACCCCTATT     | TGTTTATTT      | TCTAAATACA  |            | TATCCGCTCA |
| 161      |                | ACAAATAAAA     |             |            | ATAGGCGAGT |
| 151      |                | ACCCTGATAA     |             |            | AAGGAAGAGT |
| 201      | ACTCTGTTAT     | TGGGACTATT     |             | TTATAACTTT | TTCCTTCTCA |
| 201      | ATGAGTATTC     | <del>-</del>   |             | ATTCCCTTTT | TIGCGGCATT |
| 051      | TACTCATAAG     | TTGTAAAGGC     | ACAGCGGGAA  |            | AACGCCGTAA |
| 251      | TTGCCTTCCT     |                | ACCCAGAAAC  | GCTGGTGAAA | GTAAAAGATG |
| 201      | AACGGAAGGA     |                |             | CGACCACTTT | CATTTTCTAC |
| 301      | CTGAAGATCA     |                |             | ACATCGAACT | GGATCTCAAC |
|          | GACTTCTAGT     | CAACCCACGA     |             | TGTAGCTTGA | CCTAGAGTTG |
| 351      | AGCGGTAAGA     |                |             | GAAGAACGTT | TTCCAATGAT |
|          | TCGCCATTCT     | AGGAACTCTC     |             | CTTCTTGCAA | AAGGTTACTA |
| 401      |                | AAAGTTCTGC     |             | GGTATTATCC | CGTATTGACG |
|          | CTCGTGAAAA     |                | ATACACCGCG  |            | GCATAACTGC |
| 451      | CCGGGCAAGA     |                |             | ACTATTCTCA | GAATGACTTG |
|          |                | CGTTGAGCCA     |             | TGATAAGAGT | CTTACTGAAC |
| 501      | GTTGAGTACT     |                |             | CTTACGGATG | GCATGACAGT |
|          | CAACTCATGA     |                |             | GAATGCCTAC | CGTACTGTCA |
| 551      | AAGAGAATTA     |                |             |            | ACTGCGGCCA |
|          |                | ACGTCACGAC     |             | CTCACTATTG | TGACGCCGGT |
| 601      | ACTTACTTCT     |                |             | AGGAGCTAAC | CGCTTTTTTG |
|          | TGAATGAAGA     |                | CCTCCTGGCT  | TCCTCGATTG | GCGAAAAAAC |
| 651      | CACAACATGG     | GGGATCATGT     | AACTCGCCTT  |            | AACCGGAGCT |
|          | GTGTTGTACC     | CCCTAGTACA     | TTGAGCGGAA  | CTAGCAACCC | TTGGCCTCGA |
| 701      | GAATGAAGCC     | ATACCAAACG     | ACGAGCGTGA  | CACCACGATG | CCTGTAGCAA |
|          | CTTACTTCGG     |                | TGCTCGCACT  | GTGGTGCTAC | GGACATCGTT |
| 751      | TGGCAACAAC     | GTTGCGCAAA     | CTATTAACTG  | GCGAACTACT | TACTCTAGCT |
|          | ACCGTTGTTG     | CAACGCGTTT     | GATAATTGAC  |            | ATGAGATCGA |
| 801      | TCCCGGCAAC     | AATTAATAGA     | CTGGATGGAG  | GCGGATAAAG | TTGCAGGACC |
|          | AGGGCCGTTG     |                | GACCTACCTC  | CGCCTATTTC | AACGTCCTGG |
| 851      | ACTTCTGCGC     | TCGGCCCTTC     |             | GTTTATTGCT | GATAAATCTG |
|          | TGAAGACGCG     | AGCCGGGAAG     | GCCGACCGAC  | CAAATAACGA | CTATTTAGAC |
| 901      | GAGCCGGTGA     | GCGTGGGTCT     | CGCGGTATCA  | TTGCAGCACT | GGGGCCAGAT |
|          | CTCGGCCACT     | CGCACCCAGA     | GCGCCATAGT  | AACGTCGTGA | CCCCGGTCTA |
| 951      | GGTAAGCCCT     | CCCGTATCGT     | AGTTATCTAC  | ACGACGGGGA | GTCAGGCAAC |
|          | CCATTCGGGA     | GGGCATAGCA     | TCAATAGATG  | TGCTGCCCCT | CAGTCCGTTG |
| 1001     | TATGGATGAA     | CGAAATAGAC     | AGATCGCTGA  | GATAGGTGCC | TCACTGATTA |
|          | ATACCTACTT     | GCTTTATCTG     | TCTAGCGACT  | CTATCCACGG | AGTGACTAAT |
| 1051     |                |                |             | CATATATACT |            |
|          |                |                |             |            | AATCTAACTA |
| 1101     | TTAAAACTTC     | ATTTTTAATT     | TAAAAGGATC  | TAGGTGAAGA | TCCTTTTTGA |
|          | AATTTTGAAG     | TAAAAATTAA     | ATTTTCCTAG  | ATCCACTTCT | AGGAAAAACT |
| 1151     |                |                |             | GTTTTCGTTC |            |
|          | ATTAGAGTAC     | TGGTTTTAGG     | GAATTGCACT  | CAAAAGCAAG | GTGACTCGCA |
| 1201     |                |                |             |            | TTTTTTTCTG |
|          | GTCTGGGGCA     | TCTTTTCTAG     | TTTCCTAGAA  | GAACTCTAGG | AAAAAAAGAC |
|          |                |                |             |            |            |

| 1251 | CGCGTAATCT | CCTCCTTCCA | ААСАААААА  | CCACCCCTAC | CAGCGGTGGT |
|------|------------|------------|------------|------------|------------|
|      | GCGCATTAGA | CGACGAACGT | TTGTTTTTTT | GGTGGCGATG | GTCGCCACCA |
| 1301 | TTGTTTGCCG | GATCAAGAGC | TACCAACTCT | TTTTCCGAAG | GTAACTGGCT |
|      | AACAAACGGC |            | ATGGTTGAGA | AAAAGGCTTC | CATTGACCGA |
| 1351 | TCAGCAGAGC |            | AATACTGTCC | TTCTAGTGTA | GCCGTAGTTA |
|      | AGTCGTCTCG | CGTCTATGGT | TTATGACAGG | AAGATCACAT | CGGCATCAAT |
| 1401 | GGCCACCACT | TCAAGAACTC | TGTAGCACCG | CCTACATACC | TCGCTCTGCT |
| •    | CCGGTGGTGA |            | ACATCGTGGC | GGATGTATGG | AGCGAGACGA |
| 1451 | AATCCTGTTA | CCAGTGGCTG |            | CGATAAGTCG | TGTCTTACCG |
|      | TTAGGACAAT | GGTCACCGAC | GACGGTCACC | GCTATTCAGC | ACAGAATGGC |
| 1501 | GGTTGGACTC | AAGACGATAG | TTACCGGATA | AGGCGCAGCG | GTCGGGCTGA |
|      | CCAACCTGAG | TTCTGCTATC | AATGGCCTAT | TCCGCGTCGC | CAGCCCGACT |
| 1551 | ACGGGGGGTT | CGTGCATACA |            | GAGCGAACGA | CCTACACCGA |
|      | TGCCCCCAA  |            | CGGGTCGAAC | CTCGCTTGCT | GGATGTGGCT |
| 1601 | ACTGAGATAC | CTACAGCGTG |            | AAGCGCCACG | CTTCCCGAAG |
|      | TGACTCTATG | GATGTCGCAC | TCGATACTCT | TTCGCGGTGC | GAAGGGCTTC |
| 1651 | GGAGAAAGGC | GGACAGGTAT | CCGGTAAGCG | GCAGGGTCGG | AACAGGAGAG |
|      | CCTCTTTCCG |            |            | CGTCCCAGCC | TTGTCCTCTC |
| 1701 | CGCACGAGGG | AGCTTCCAGG |            | TGGTATCTTT | ATAGTCCTGT |
|      | GCGTGCTCCC | TCGAAGGTCC | CCCTTTGCGG | ACCATAGAAA | TATCAGGACA |
| 1751 | CGGGTTTCGC | CACCTCTGAC | TTGAGCGTCG | ATTTTTGTGA | TGCTCGTCAG |
|      | GCCCAAAGCG | GTGGAGACTG |            | TAAAAACACT | ACGAGCAGTC |
| 1801 | GGGGGCGGAG |            | AACGCCAGCA | ACGCGGCCTT | TTTACGGTTC |
|      | CCCCCGCCTC | GGATACCTTT | TTGCGGTCGT | TGCGCCGGAA | AAATGCCAAG |
| 1851 | CTGGCCTTTT | GCTGGCCTTT | TGCTCACATG | TTCTTTCCTG | CGTTATCCCC |
|      | GACCGGAAAA | CGACCGGAAA | ACGAGTGTAC | AAGAAAGGAC | GCAATAGGGG |
| 1901 | TGATTCTGTG | GATAACCGTA | TTACCGCCTT | TGAGTGAGCT | GATACCGCTC |
|      | ACTAAGACAC | CTATTGGCAT | AATGGCGGAA | ACTCACTCGA | CTATGGCGAG |
| 1951 | GCCGCAGCCG | AACGACCGAG | CGCAGCGAGT | CAGTGAGCGA | GGAAGCGGAA |
|      | CGGCGTCGGC | TTGCTGGCTC | GCGTCGCTCA | GTCACTCGCT | CCTTCGCCTT |
| 2001 | GAGCGCCCAA | TACGCAAACC | GCCTCTCCCC | GCGCGTTGGC | CGATTCATTA |
|      | CTCGCGGGTT | ATGCGTTTGG | CGGAGAGGGG | CGCGCAACCG | GCTAAGTAAT |
| 2051 | ATGCAGCTGG | CACGACAGGT | TTCCCGACTG | GAAAGCGGGC | AGTGAGCGCA |
|      | TACGTCGACC |            | AAGGGCTGAC | CTTTCGCCCG | TCACTCGCGT |
| 2101 | ACGCAATTAA | TGTGAGTTAG | CTCACTCATT | AGGCACCCCA | GGCTTTACAC |
|      | TGCGTTAATT | ACACTCAATC | GAGTGAGTAA | TCCGTGGGGT | CCGAAATGTG |
| 2151 | TTTATGCTTC | CGGCTCGTAT | GTTGTGTGGA |            | GATAACAATT |
|      | AAATACGAAG | GCCGAGCATA | CAACACACCT | TAACACTCGC | CTATTGTTAA |
| 2201 | TCACACAGGA |            | ACCATGATTA |            | GCATGCAAAT |
|      | AGTGTGTCCT | TTGTCGATAC | TGGTACTAAT | GCGGTTCGAA | CGTACGTTTA |
| 2251 | TCTATTTCAA |            | ATAATGAAAT | ACCTATTGCC | TACGGCAGCC |
|      | AGATAAAGTT | CCTCTGTCAG | TATTACTTTA | TGGATAACGG | ATGCCGTCGG |
| 2301 | GCTGGATTGT |            |            | GCCATGGCCC | AGGTGCAGCT |
|      | CGACCTAACA | ATAATGAGCG |            | CGGTACCGGG | TCCACGTCGA |
| 2351 | GCAGGTCGGC | CTCGAGATCA |            | CGCAGGTGCG | CCGGTGCCGT |
| 2403 | CGTCCAGCCG |            | TTGCCCGCCG | GCGTCCACGC | GGCCACGGCA |
| 2401 | ATCCAGATCC | GCTGGAACCG | CGTGGGGCCG | CAAGCGCTTG | GAGCCACCCG |
| 2451 | TAGGTCTAGG | CGACCTTGGC | GCACCCGGC  | GTTCGCGAAC | CTCGGTGGGC |
| 2451 | CAGTTCGAAA | AATAATAAGG | ATCCGAATTC | ACTGGCCGTC | GTTTTACAAC |
|      | GTCAAGCTTT | TTATTATTCC | TAGGCTTAAG | TGACCGGCAG | CAAAATGTTG |

| 0501              |            |            |            |            |            |
|-------------------|------------|------------|------------|------------|------------|
| 2501              | GTCGTGACTG | GGAAAACCCT | GGCGTTACCC | AACTTAATCG | CCTTGCAGCA |
|                   | CAGCACTGAC | CCTTTTGGGA | CCGCAATGGG | TTGAATTAGC | GGAACGTCGT |
| 2551              | CATCCCCCTT | TCGCCAGCTG | GCGTAATAGC | GAAGAGGCCC | GCACCGATCG |
|                   | GTAGGGGGAA | AGCGGTCGAC | CGCATTATCG | CTTCTCCGGG | CGTGGCTAGC |
| 2601 <sub>.</sub> | CCCTTCCCAA | CAGTTGCGCA | GCCTGAATGG | CGAATGGCGC | CTGATGCGGT |
|                   | GGGAAGGGTT | GTCAACGCGT | CGGACTTACC | GCTTACCGCG | GACTACGCCA |
| 2651              | ATTTTCTCCT | TACGCATCTG | TGCGGTATTT | CACACCGCAT | ACGTCAAAGC |
|                   | TAAAAGAGGA | ATGCGTAGAC | ACGCCATAAA | GTGTGGCGTA | TGCAGTTTCG |
| 2701              | AACCATAGTA | CGCGCCCTGT | AGCGGCGCAT | TAAGCCCGGC | GGGTGTGGTG |
|                   | TTGGTATCAT | GCGCGGGACA | TCGCCGCGTA | ATTCGGGCCG | CCCACACCAC |
| 2751              | GTTACGCGCA | GCGTGACCGC | TACACTTGCC | AGCGCCCTAG | CCCCCGCTCC |
|                   | CAATGCGCGT | CGCACTGGCG | ATGTGAACGG | TCGCGGGATC | GGGGGCGAGG |
| 2801              | TTTCGCTTTC | TTCCCTTCCT | TTCTCGCCAC | GTTCGCCGGC | TTTCCCCGTC |
|                   | AAAGCGAAAG | AAGGGAAGGA | AAGAGCGGTG | CAAGCGGCCG | AAAGGGGCAG |
| 2851              | AAGCTCTAAA | TCGGGGGCTC | CCTTTAGGGT | TCCGATTTAG | TGCTTTACGG |
|                   | TTCGAGATTT | AGCCCCCGAG | GGAAATCCCA | AGGCTAAATC | ACGAAATGCC |
| 2901              | CACCTCGACC | CCAAAAAACT | TGATTTGGGT | GATGGTTCAC | GTAGTGGGCC |
|                   | GTGGAGCTGG | GGTTTTTTGA | ACTAAACCCA | CTACCAAGTG | CATCACCCGG |
| 2951              | ATCGCCCTGA | TAGACGGTTT | TTCGTCCTTT | GACGTTCGAG | TCCACGTTCT |
|                   | TAGCGGGACT | ATCTGCCAAA | AAGCAGGAAA | CTGCAAGCTC | AGGTGCAAGA |
| 3001              | TTAATAGTGG | ACTCTTGTTC | CAAACTGGAA | CAATACTCAA | CCCTATCTCG |
|                   | AATTATCACC | TGAGAACAAG | GTTTGACCTT | GTTATGAGTT | GGGATAGAGC |
| 3051              | GGCTATTCTT | TTGATTTATA | AGGGATTTTG | CCGATTTCGG | CCTATTGGTT |
|                   | CCGATAAGAA | AACTAAATAT | TCCCTAAAAC | GGCTAAAGCC | GGATAACCAA |
| 3101              | AAAAAATGAG | CTGATTTAAC | AAAAATTTAA | CGCGAATTTT | AACAAAATAT |
|                   | TTTTTTACTC | GACTAAATTG | TTTTAAATT  | GCGCTTAAAA | TTGTTTTATA |
| 3151              | TAACGTTTAC | AATTTTATGG | TGCAGTCTCA | GTACAATCTG | CTCTGATGCC |
|                   | ATTGCAAATG | TTAAAATACC | ACGTCAGAGT | CATGTTAGAC | GAGACTACGG |
| 3201              | GCATAGTTAA | GCCAGCCCCG | ACACCCGCCA | ACACCCGCTG | ACGCGCCCTG |
|                   | CGTATCAATT | CGGTCGGGGC | TGTGGGCGGT | TGTGGGCGAC | TGCGCGGGAC |
| 3251              | ACGGGCTTGT | CTGCTCCCGG | CATCCGCTTA | CAGACAAGCT | GTGACCGTCT |
|                   | TGCCCGAACA | GACGAGGGCC | GTAGGCGAAT | GTCTGTTCGA | CACTGGCAGA |
| 3301              | CCGGGAGCTG | CATGTGTCAG | AGGTTTTCAC | CGTCATCACC | GAAACGCGCG |
|                   | GGCCCTCGAC | GTACACAGTC | TCCAAAAGTG | GCAGTAGTGG | CTTTGCGCGC |
| 3351              | A          |            |            |            |            |
|                   | T          | •          |            |            |            |
|                   |            |            |            |            |            |

Fig. 8b

cDNA primers

| VLK-c   | CTGGATGGTGGGAAGATGGA           |
|---------|--------------------------------|
| VLL-c   | TCAGAGGAAGGAACAGGGT            |
| IgG1-c  | CTTACAACCACAATCCCTGGGCACAATTTT |
| IgG2a-c | CTTTGTGGGCCCTCTGGGCTCAAT       |
| lgG2b   | TGAAATGGGCCCGCTGGGCTCAAG       |
| lgG3-c  | GGGCTTGGGTATTCTAGGCTCGAT       |

VH forward primers without restriction sites

| M-VH1 | GAGGTGCAGCTTCAGGAGTCAGG |
|-------|-------------------------|
| M-VH2 | CAGGTGCAGCTGAAGGAGTCAGG |
| M-VH3 | GAGGTCCAGCTGCAACAGTCTGG |
| M-VH4 | GAGGTTCAGCTGCAGCAGTCTGG |
| M-VH5 | CAGGTCCAACTGCAGCCTGG    |
| M-VH6 | CAGGTTCAGCTGCAGCAGTCTGG |
| M-VH7 | GAGGTGAAGCTGGTGGAGTCTGG |
| M-VH8 | GAGGTGAAGCTGGTGGAATCTGG |
| M-VH9 | GAGGTTCAGCTCTGG         |

VH backward primers without restriction sites

| M-JH1 | TGAGGAGACGGTGACCGTGGTCCC |  |
|-------|--------------------------|--|
| M-JH2 | TGAGGAGACTGTGAGAGTGGTGCC |  |
| M-JH3 | TGCAGAGACAGTGACCAGAGTCCC |  |
| M-JH4 | TGAGGAGACGGTGACTGAGGTTCC |  |

VL forward primer without restriction sites

| , 2 101 |                         |  |
|---------|-------------------------|--|
| M-VK1   | GACATTGTGATGACACAGTCTCC |  |
| M-VK2   | GATGTTGTGATGACCCAAACTCC |  |
| M-VK3   | GATATCCAGATGACACAGACTCC |  |
| M-VK4   | CAAATTGTTCTCACCCAGTCTCC |  |
| M-VL1   | CAGGCTGTTGTGACTCAGGAATC |  |

VL backward primers without restriction sites

| M-JK1 | TTTGATTTCCAGCTTGGTGCCTCC |
|-------|--------------------------|
| M-JK2 | TTTTATTTCCAGCTTGGTCCCCCC |
| м-ЈКЗ | TTTCAGCTCCAGCTTGGTCCCAGC |
| M-JL1 | ACCTAGGACAGTGACCTTGGTTCC |



VH forward primers with restriction sites

| VIIIOIWaid | primers with restriction sites                           |
|------------|--|
| MVH1 Sfil  | GTCCTCGCAACTGCGGCCCAGCCGGCCATGGCCGAGGTGCAGCTTCAGGAGTCAGG |
| MVH2 Sfil  | GTCCTCGCAACTGCGGCCCAGCCGGCCATGGCCCAGGTGCAGCTGAAGGAGTCAGG |
| MVH3 Sfil  | GTCCTCGCAACTGCGGCCCAGCCGGCCATGGCCGAGGTCCAGCTGCAACAGTCTGG |
| MVH4 Sfil  | GTCCTCGCAACTGCGGCCCAGCCGGCCATGGCCGAGGTTCAGCTGCAGCAGTCTGG |
| MVH5 Sfil  | GTCCTCGCAACTGCGGCCCAGCCGGCCATGGCCCAGGTCCAACTGCAGCAGCCTGG |
| MVH6 Sfil  | GTCCTCGCAACTGCGGCCCAGCCGGCCATGGCCCAGGTTCAGCTGCAGCAGTCTGG |
| MVH7 Sfil  | GTCCTCGCAACTGCGGCCCAGCCGGCCATGGCCGAGGTGAAGCTGGTGGAGTCTGG |
| MVH8 Sfil  | GTCCTCGCAACTGCGGCCCAGCCGGCCATGGCCGAGGTGAAGCTGGTGGAATCTGG |
| MVH9 Sfil  | GTCCTCGCAACTGCGGCCCAGCCGGCCATGGCCGAGGTTCAGCTTCAGCAGTCTGG |
|            |  |

VH backward primers with restriction sites

| MJH1 Sall | GAGTCATTCTCGTGTCGACACGGTGACCGTGGTCCC |             |
|-----------|--------------------------------------|-------------|
| MJH2 Sali | GAGTCATTCTCGTGTCGACACTGTGAGAGTGGTGCC | <del></del> |
| MJH3 Sall | GAGTCATTCTCGTGTCGACACAGTGACCAGAGTCCC |             |
| MJH4 Sall | GAGTCATTCTCGTGTCGACACGGTGACTGAGGTTCC |             |

VL forward primers with restriction sites

|            | P  |  |
|------------|--|--|
| MVK1 ApaL1 | TGAGCACAGTGCACTCGACATTGTGATGACACAGTCTCC    |  |
| MVK2 ApaL1 | TGAGCACACAGTGCACTCGATGTTGTGATGACCCCAAACTCC |  |
| MVK3 ApaL1 | TGAGCACACTGCACTCGATATCCAGATGACACAGACTCC    |  |
| MVK4 ApaL1 | TGAGCACAGTGCACTCCAAATTGTTCTCACCCAGTCTCC    |  |
| MVL1 ApaL1 | TGAGCACACAGTGCACTCCAGGCTGTTGTGACTCAGGAATC  |  |

VL backward primers with restriction sites

| M-JK1 Not1 | GAGTCATTCTCGACTTGCGGCCGCTTTGATTTCCAGCTTGGTGCCTCC |
|------------|--|
| M-JK2 Not1 | GAGTCATTCTCGACTTGCGGCCGCTTTTATTTCCAGCTTGGTCCCCCC |
| M-JK3 Not1 | GAGTCATTCTCGACTTGCGGCCGCTTTCAGCTCCAGCTTGGTCCCAGC |
| M-JL1 Not1 | GAGTCATTCTCGACTTGCGGCCGCACCTAGGACAGTGACCTTGGTTCC |

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| Polypeptide | SEQ ID No. | Protein Sequence  | SEQ ID No. of           |
|-------------|------------|---|-------------------------|
| or NPB      |            |   | the CDK 3 as underlined |
| scFv1       | . 1        | 1 EVQLQQSGPE LVKPGALVKI SCKASGYTVT SYDINWVKQR PGQGLEWIGW 51 IYPGDGSTKY NEKEKGKATL TVDKSSTTVY MQLSSLTSEN SAVYFCARGG 101 KYFDYWGQGT TLTVSTGGGG SGGGSGGGG SALDIVMTQS PKFMSTSVGD 151 RVSVTCKASQ NVATNVAWYQ QKPGQSPKPL TYSASFRSSG VPDRFTGSGS 201 GTDFTLTISN VQSEDLAEYF CQQYNSYPYT FGGGTKLEIK AAAGAPVPYP 251 DPLEPRGAAS AWSHPQFEK*                      | 73                      |
| scFv2       | . 2        | 1 EVQLLESGGG LVQPGGSLRL SCAASGETES SYAMSWVRQA PGKGLEWVSA 51 ISGSGGSTYY ADSVKGRETI SRDNSKNTLY LQMNSLRAED TAVYYCARDS 101 GLQQGPRRRG ARVNFSYYGL DVWGRGTTVT VSSGGGGSGG GGSGGGSAQ 151 AVLTQPSSAS GTPGQRVTIS CSGSNSNIGR NYVEWYQQFP GTAPKILIYR 201 NNQRPSGVPD RESGSKSGTS ASLAISGLRS EDEADYYCAS WDDSLTWVFG 251 GGTKVTVLGA AAGAPVPYPD PLEPRGAASA WSHPQFEK* | 74                      |
| scFv3       |            | 1 ASVKVSCKTS GYTEIAYYIH WVRQAPGQGL EWMGRINPNT GGINLAQKFQ 51 GRVTVTRDTS ISTAHMELSR LSSDDTAVYY CARERIVPAG LRNRGMYTAV 101 GMDVWGRGTL VTVSSGGGG GGGGSGGGS AQSVVTQPPS MSGTPGQRVT 151 ISCSGSRSNI GRNYVYWYQQ FPGTAPKLLI YRNNERPSGV PDRFSASKSG 201 TSASLAISGL RSEDEADYYC ATWDDSLSGT WVFGGGTKLT VLGAAA   | 75                      |
| scFv4       | 9          | 1 LLESGGGLVQ PGGSLRLSCA ASGFTESSYA MSWVRQAPGK GLEWVSAISG 51 SGGSTYYADS VKGRFTISRD NSKNTLYLQM NSLRAEDTAV YYCARGGGRY 101 DSSHGFDSWG RGTMVTVSSG GGGSGGGGG GGGSALSYEL TQPPSVSVAP 151 GETATITCGG RSLGSKVVHW YQQKPGQAPT LVIYYDSVRP SGVPERFSAS 201 NSRLSATLTV SRVEAGDEAD YYCQVWDRSS DHYVFGTGTK LTVLGAAA  | 76                      |
| scFv5       |            | 1 QLLESGGGLV QPGGSIRLSC AASGFTESSY AMSWVRQAPG KGLEWVSAIS 51 GSGGSTYYAD SVKGRFTISR DNSKNTLYLQ MNSLRAEDTA VYYCARDWRW 101 QQFGGWFDPW GRGTLVTVSS GGGGSGGGS GGGGSALETT LTQSPATLSL 151 SPGETATLEC RASQSVRNNL VWYQQKLGQA PRLLIFGAST RASGIPDRFT 201 GSGSGTDFSL TITKLEPEDE AVYYCQRYGG FPITFGQGTR LEIKRAAA  | 77                      |
| scFv6       | 8          | 1 QLVQSGGGLV QPGGSLRLAC EASGFRFSSY GMSWVRQAPG KGLEWVSSMS<br>51 DSGANTYYAD SVKGRFTISR DNAKKMLYLQ MSSLRGEDTA VYYCATLFRG<br>101 SGYVRHWGRG TLVTVSSGGG GSGGGGGGG GSAQAVLTQP SSASGTPGQR  | 78                      |

| GSK   | NYA                                | PSY 79                             |                                   | SGS                                | А                                | LEW                                | CAR 80                   |                                  | ESG                                |                                 | SAN                                | RTY 81                             |                           | SDS                                |                                | VKG                                | OIY 82                   |                           | GSK                       | A                                | TIX                     | EKM 83                   |                           | GSD                   |                           | GTA                     | ERG 84                   |                                   | SGS                                | А                                | EIX                     | WNH 85                   |                      | FSA                       | _                                 |
|---|------------------------------------|------------------------------------|-----------------------------------|------------------------------------|----------------------------------|------------------------------------|--------------------------|----------------------------------|------------------------------------|---------------------------------|------------------------------------|------------------------------------|---------------------------|------------------------------------|--------------------------------|------------------------------------|--------------------------|---------------------------|---------------------------|----------------------------------|-------------------------|--------------------------|---------------------------|-----------------------|---------------------------|-------------------------|--------------------------|-----------------------------------|------------------------------------|----------------------------------|-------------------------|--------------------------|----------------------|---------------------------|-----------------------------------|
| Y QQLPGTAPKL LISKNSRRPS GVPDRFSGSK<br>Y YCAAWDDRLS GPAFGGGTKL TVLGAAA | S YAISWVRQAP GOGLEWMGGI IPMSGIPNYA | M ELSSLRSEDT AVYYCARGGR YVDFGRGPSY | G GGSGGGSGG GGSAQSVLTQ PPSASGTPGQ | W YHQLPGTAPK LLIYRNDQRP SGVPDRFSGS | D YYCAAWDDNL SGLFFGGGTK LTVLGAAA | S LNCTVSGSSL SSGGYYWSWI RQHPGKGLEW | TISVDISKNO FSLKLSSVTA    | S SGGGGSGGG SGGGSDIQM TQSPSTLSAS | A WYQQKPGKAP KLLIYKASSL ASGAPSRFSG | A TYYCQOYSNY PLTFGGGTKL EIKRAAA | F NSYALNWVRQ APGOGLEWMG GIIPIFGSAN | A YLELSSLRSE DTAVYYCARA LHLDYVWRTY | GSGGGGSGGG GSALSSELTQ     | Q QKPGQAPVLV IYGKNSRPSG IPDRFSGSDS | Y CNSRDRSGNR VVFGGGTKLT VLGAAA | W VROAPGKGLE WVSAISGSGG STYYADSVKG | RAEDTAVYYC ARGVTYHYDH    | GSGGGGSGG GSAQAVLTQP      | QQLPGTAPKL LIYRNNQRPS     | Y YCAARDNGLS AYVIFGGGTK LTVLGAAA | NYWIAWVROM PGKGLEWMGI   | LOWSSLKASD TAMYYCAROG    | SGGGGSGGG SALSYELTQP      | QQLPGTAPKV LISSDNQRPS | YCAAWDDSLS AYVFGSGTKL     | FSYNAINWVR QAPGOGLEWM   | AYMELTRIRS EDTAMYYCAR    | G GGSGGGSGG GGSALPVLTQ PPSASGAPGQ | W YKQLPGTAPK LFIYKNDQRP SGVPDRFSGS | D YYCLTWDDSL SGPVFGGGTK LTVLGAAA | VSGGSINNNN WWSWVRQPPG   | KSNNQFSLKM SSVTAADTAV    | GGGSGGGSG GGGSAQSVLT |                           | A DYYCAAWDDR RVVFGGGTKI, TVI,GAAA |
| 151 VIISCSGSSS NIASNYVYWY<br>201 SGTSASLAIS ELRSEDEADY                | 1 KKPGSSVKVS CKASGGTFSS            | 51 QKFQDRVTIT ADKSTSTAYM           | 101 HYYYMDVWGR GTLVTVSSGG         | 151 RVTISCSGAT SNIGRNYVYW          | 201 KSGTSASLAI SGLRSDDEAD        | 1 AQVQLQQWGP GLVKASEILS            | 51 IGYIHYSGST YYNPSLKSRV | 101 VPLREDGEDV WGQGTLVTVS        | 151 IGDRVTITCR ASEGIYHWLA          | 201 SGSGTDFTLT ISSLQPDDFA       | 1 ELKKPGSSVK VSCKAPRGTF            | 51 YAPKFQGRVT ITADESTITA           | 101 NYYEDNWGKG TMVTVSSGGG | 151 TVRITCQGDS LRSYYASWYQ          | 201 GNTASLTITG AQAEDEADYY      | 1 SLRLSCAASG FTFSSYAMSW            | 51 RFTISRDNSK NTLYLQMNSL | 101 NHGLDVWGRG TTVTVSSGGG | 151 VTISCSGSSS NIGKNYVYWY | 201 SGTSASLAIS GLRSEDEADY        | 1 VKKPGESLKI SCKGSGYSFP | 51 SPSFRGQVTI SADKSISTAY | 101 YASDIWGRGT LVTVSSGGGG | -                     | 201 SGTSASLVIS RLRFEDEGDY | 1 AEVKKPGSSV RVSCKASGDT | 51 KQAQKFQGRV TFTADESTST | 101 YYYHMDVWGQ GTLVTVSSGG         | 151 RITISCSGST FNIGRNYVDW          | 201 KSGTSASLVV SGLRSEDEAD        | 1 LQESGPGLVK PSGTLSLTCA | 51 QSGSTNYNPS LKSRVTISVD | GPYYGMDVWG           | 151 QRVTISCSGS SSNIGSNEVY | COCCEDENT TOCT DOPPEN             |
|   | 6                                  |                                    |                                   |                                    |                                  | 10                                 |                          |                                  |                                    |                                 |                                    |                                    |                           |                                    | •                              | 12                                 | <br>!                    |                           |                           |                                  | 13                      | <u> </u>                 |                           |                       |                           | 14                      |                          |                                   |                                    |                                  | 15                      | 3                        |                      |                           |                                   |
|   | crFv7                              |                                    |                                   |                                    |                                  | scFv8                              | )                        |                                  |                                    |                                 | scFv9                              |                                    |                           |                                    |                                | scFv10                             |                          |                           |                           |                                  | scFv11                  |                          |                           |                       |                           | scFv12                  |                          |                                   |                                    |                                  | scFv13                  |                          |                      |                           |                                   |

| 16  | VQLQESGPGL VKPSETLSLT CTVSGGPVAS SSYYWGFIRQ PPGKGLEWIG  |
|-----|---|
| 101 | TLVTVSSGGG GSGGGGSGGG                                   |
| 151 | QRISSYLNWY QQKPGKAPKL LIYAASSLQS                        |
| 201 | SGTDFTLTIS SLQPEDFATY YCQQSYSTPI TFGQGTRLEI KRAAA       |
| 1   |   |
| 51  | SGGSTYYADS VKGRFTISRD NSKNTLYLQM NSLRAEDTAV YYCARDWRWQ  |
| 101 |   |
| 151 | ASQSVGSKLA WYQQKPGQAP RLLIFGTSTR                        |
| 201 | ISSLQSEDFA VYYCQQYNNW PPYTFGQGTK                        |
| _   | KVSCKASGYR FETYGESWVR QAPGQGLEWM                        |
| 51  | TMTTDTSTST AYMELRSLRS DDTAVYFCSR                        |
| 101 | TIVIVSSGGG GSGGGGGGG GSAQSVLIQP                         |
| 151 | NIGSNYVYWY QQLPGTAPKL LIHKNNRRPS                        |
| 201 | GLRSEDEADY  |
| -   |   |
| 51  | KGRFTISRDN SKNTLYLQMN SLRAEDTAVY                        |
| 101 | FGGWFDPWGR GTMVTVSSGG GGSGGGGGGGGGGGGALETTLT QSPGTLSLSP |
| 151 | GDRATLSCRA SHSVSHNHLA WYQQNPGQAP RLLIFGASSR AAGIPDRFSG  |
| 201 | SGSGTDFTLT ISRLEPEDFA SYYCOOYGSP RRTFGOGTKV EIKRAAA     |
| H   | CKAPGGTFGN  |
| 21  |   |
| 101 | TLVTVSSGGG GSGGGGGGG GSAQSVLTQP                         |
| 151 |   |
| 201 | _   |
| 1   | KKPGSSVKVS CKASGGTFSS                                   |
| 51  | OKFOGRVIII ADKSTTTAYM ELTSLRFEDA                        |
| 101 | TLVTVSSGGG GSGGGGGGG GSALSSELTQ                         |
| 151 | LTSYYAAWYQ QKPGQAPLLV FYGKDKRPSG                        |
| 201 | 1   |
| Н   | KKPGSSVKVS CKASGCTFTS YAISWVRQAP GOGLEWMGGF IPVFGTANYA  |
| 51  |   |
| 101 | YYMDVWGQGT MVTVSSGGG SGGGGSGGG SAQSVLTQPP AASGTYGQKI    |
| 151 | TISCSGSSSN IGVNYVYWYR QFPGAAPHVV IYNNDQRPSG VPDRFSGSKS  |
| 201 | GTSASLAISG LRSEDEADYY CSTWDDTLSG YIFGVGTKVT VLGAAA      |
| 1   | AASGETESSY AMSWVRQAPG KGLEWVSAIS                        |
| 51  | SVKGRFTISR DNSKNTLYLQ MNSLRAEDTA VYYCARDWRW QQFGGWFDPW  |

Fig. 10

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| WQPGGSIRLS CAASCETESS YAMSWURGAP GKGLEWVSAI  BSVKGRETIS RDNSKNTLYL OMNSLRAEDT AVYYCARDHR RPLDYWGQGT WVTVSSGGGG SGGGGSGGG SALPVLTQPP TISCSGSSSN IGRNYVYWYQ QLPGTAPKLL IYRNNIRPSG GTSASLAISG IRSEDEADYY CAAWDDTILSG VVEGGTKLT EVRRPGASVK ISCKASGETF TSYLEHWVRQ APGQRLEWWG YSPKEQGRYT LTGDTSTSTT YMELSSITSE DTAVYYCARD IRPSEDEWGR GTLVTVSSG GGSGGGSGG GGSDIQMTQS RVTITCRASE GIYHMLAWYQ QKPGKAPKLL IYKASSLASG GTDFTLTISS LQPDDEATYY CQQYSNYPLT EGGSTKLEIK VRPGGSIRLS CAASGETEDD YGMSWURQAP GKGLEWVSYG DSVKGRFTIS RDNAKNSLYL OINSLRAEDT AVYYCARRYY VTVSSGGGG GGGGGGGGG ALSTELTQDP ATVYVCARRY VTVSSGGGG GGGGGGGGG ALSTELTQDP ATVYVCARRY CMDVWGRGFT SRDNANNSLY LQMNSLTAEDT TAVYYCARRY ADSVKGRFTI SRDNANNSLY LQMNSLTAEDT TAVYYCARRY CMDVWGRGFT VTVSSGGGG GGGGGGGGG ALPVITQPPS ISCSGSSSNI GSNTLNWYQQ LPGTAPKLLI YSNDQRPSGV ISCSGSSNI GSNTLNWYQQ LPGTAPKLLI YSNDQRPSGV ISCSGSSNI GSNTLNWYQQ LPGTAPKLLI YSNDQRPSGV ISCSGGGSSOG GGGGGGGGGG GGGGGGGGG GGGGGGGGG GGGGGG  |        |      | 201      | EDEADYYCNS RDSSGNHIVE GGGTKI.TVI.G. JABA |     |
|--|--------|------|----------|--|-----|
| 101   RELDÍNGGET MUYUSSGGG SGGGGGGGG SALPUTORP   101   TELDÍNGGGT MUYUSSGGG SGGGGGGGG SALPUTORP   115   TESCESSSN TERNAVYTWYO QLECTA-RELL IYANURESC   151   TESCESSSN TERNAVYTWYO QLECTA-RELL IYANURESC   151   TENETEDEMOR TICHTVYNYO QLECTA-RELL IYANURESC   151   TENETEDEMOR TICHTVANYO GREGGGGGGG GGSDUGGTENG   151   RATETTRA-BE GASGETED VORSCAGGGG GGSDUGGGGGG GGSDUGMOS   151   RATETTRA-BE GASGETED VORSCAGGGG GGSDUGMOS   151   NYDROSCAGGS GGGGGGGGG GGSDUGMOS   151   DEVYGRETIS RODARANILY CONSNIVELT EGGCTKLEIK   101   TUVORGGSIRLS GASGETED VORSCARRYROR EGGCTKLEIK   101   TUVORGGSIRLS GASGETED VORSCARRYROR EGGCTKLEIK   101   TUVORGGSIRL SCAAGGTED VORSCARRYROR EGGCTKLEIK   101   TUVORGGSIRL SCAAGGTETED TEMNAVAGA PGGCTKVIVOR   151   DEVYGRETI SRDNAKNILY LOMNSITABD TAVYCARREY   101   TAVSCAGGG GGGGGGGGG ALSSELTORD ATVSCARRY   101   TAVSCAGGG GGGGGGGGG ALSSELTORD ATVSCARRY   101   GMDVMGRGTT VTVSSGGGG GGGGGGGG ALPVITORPS   101   SASGETED SCAAGGTETE TEMNAVAQA PGGGTKVIV   101   SASGETES AESWURQAR GGGGGGGG ALPVITOR SCAAGGTET   101   VSSGGGGGG GGGGGGGG ALPVITOR RELEATING TRANDAR   101   VSSGGGGGG GGGGGGGG ALPVITOR RELEATING TRANDAR   101   VSSGGGGGG GGGGGGGG SULPHOTOR   101   VSSGGGGG GGGGGGG SULPHOTOR   102   SGCGGGGGG CSGGGGGG CSGGGGGG CSGGGGG CSGGGGG CSGGGGG CSGGGGG CSGGGGGG CSGGGGGG CSGGGGG CSGGGGGG CSGGGGGGG CSGGGGGG CSGGGGGGG CSGGGGGGG CSGGGGGG CSGGGGGG CSGGGGGGG CSGGGGGGG CSGGGGGGG CSGGGGGGG CSGGGGGGGG   | scFv29 | 31   | H        | CAASGFTFSS YAMSWVRQAP GKGLEWVSAI         |     |
| 101   RPLDYWGOGT WYTVSGGGG SGGGSGGGG SALPVLTOPP   151   TISCSGSSN IGNIVYWYQ QLPGTAPKLL IYRNUIRPSG   201   GTSASILAISG IERBEBADYY CAAMDDTISG VVFGGGTKLT   1   EVRRPGASVK ISCKASGETF TSYLEHWYQ APGQELEWWG   101   RPSEPEWGR GTILVTVSSGG GGSGGGGGG GGSDIQWTOS   151   RVTTCRASS GIVHULAWYQ QLPGTAPKLL IYRASSLASG   201   RPGGSLRLS CAASGFTED Y CQDYSNYPLT EGGSTLEIK   101   CAPTATYWQ CPGQAPLLVF FSERIRPSGI PDRFSGSNG   201   VVSSGGGGS GGGGGGGGG AGGGSGGGG AGGTWGCT   151   DVVTATYWQ CPGQAPLLVF FSERIRPSGI PDRFSGSNG   201   CAPTATYWQ CPGQAPLLVF FSERIRPSGI PDRFSGSNG   201   CAPTATYWQ CPGGAPLLVF FSERIRPSGI PDRFSGSNG   201   CAPTATYGAP   201   CAPTATYGAP  |        |      | 51       | RDNSKNTLYL OMNSLRAEDT AVYYCARDHR         | 101 |
| 151 TISCGGSSN IGNNYVWOQ QLECTARKLI IYRNNIARBG   1  |        |      | 101      | MVTVSSGGGG SGGGGGGGG SALPVLTQPP          |     |
| 201   GTSASLAISG IRREDEADLY CAMADDTLSG VVEGGGTKIT   1  |        |      | 151      | IGRNYVYWYQ QLPGTAPKLL                    |     |
| 12 EVRKPGASVK ISCKASGFTF TSYLFHWVRQ APGQRLEWWG 101 IRPSEDEWGR GTLVTVSSGG GGSGGGGG GGSDIQWTQS 151 STYTITGRASE GTYMTLAWYQ QRPGKAPKLL IYRASSLASG 201 GTDFTLTISS LQPDPATYY CQQYSNYPTF FGGGTKLEIY 1 VRPGGSLRLS CAASGFTEDD YGWSWVRQAP GKGLEWVSGI 201 VTVSSGGGS GGGSGGGGG ALSSELTQDP ATVSYLAGGT 151 DSVKGRFTIS RDNAKNSLYL QINSLRAEDT AVYYCARRRY 101 VTVSSGGGS GGGSGGGGG ALSSELTQDP ATVSYLAGGT 201 LVQPGGSLRL SCAAAGFTES TFEMNWYRQA PGKCLEWVSY 202 ADSVKGRFTI SRDNANNSLY LQMNSLTAED TAVYYCARRK 101 GMDWGRGTT VTVSSGGGS GGGSGGGGS ALPVLTQPPS 151 ISCSGSSNI GSWTLNWYQQ LRCTARKLLI YSNDQRPSGYVTW 201 TSASLAISGL QSEDEADYYC AAWDDSLNGW VFGGGTKVTV 202 TSASLAISGL QSEDEADYYC AAWDDSLNGW VFGGGTKVTV 203 RASGGTSSS AFSWVRQAPG GGLQWMGGII PLFGAANYAQ 204 EDBADYYCLY WDDSLSGAPS GCGCKGGG GGGGGGGG ALPVLTAFS 205 EDBADYYCLY WDDSLSGAPS GTKTTVTG AAP 206 EDBADYYCLY WDDSLSGAPS GTKTTVTG AAP 207 EDBADYYCLY WDDSLSGAPS GTKTTVTG AAP 208 EDBADYYCLY WDDSLSGAPS GTKTTVTG AAP 209 GGSGGGGGGG GGGGGGSAQ SVLTQLPSAS GAPGQRITTS 201 EDBADYYCLY WDDSLSGAPY GGGKKTTTG AAP 201 EDBADYYCLY WDDSLSGAPY GGGKKTTTG AAP 202 EDBADYYCLY WBLSLTSDD TAVYYCARGG ETTATHRSRR 203 EDBADYYCKTY WBLSLTSDD TAVYYCARGG GTRATHRSRR 204 EDBADYYCKTY MDSLSGAPY GGGKKTTTTG GTRATHRSRR 205 SGGSGGGGSAQ SGGGGSGG GGGGGGSAQ GGGGGGSAQ GGGGGGSAQ GGGGGGSAQ GGGGGGGGGG   |        |      | 201      | LRSEDEADYY CAAWDDTLSG VVEGGGTKLT         |     |
| 101 IRPSEPEWGR GTLYTYSSGG GGGGGGGG GGSDIQWTOS 101 IRPSEPEWGR GTLYTYSSGG GGGGGGGG GGSDIQWTOS 101 UVRPGGSLRLS CAAGGFTEDD YGMSWTRAPT FGGGTLEREY 1 UVRPGGSLRLS CAAGGFTEDD YGMSWTRAPT GGGTLWETK 101 UVRSGGGG GGGGGGGGG ALSSLTOPD AVYCARRRY 102 UVYSSGGGG GGGGGGGGG ALSSLTOPD AVYCARRRY 103 UVYSSGGGG GGGGGGGGG ALSSLTOPD AVYCARRRY 104 UVRPGGSLRL SCAAGFTES TERMWNYGA PGREEWVST 1 LUQPGGSLRL SCAAGFTES TERMWNYGA PGREEWVST 1 LUQPGGSLR SCAAGFTES TERMWNYGA PGREEWVST 1 LUQPGGSLR SCAAGFTES TERMWNYGA PGREEWVST 1 LYGPGGSLR GSWTLWYCO LGAAG 1 LYGPGGSLR GSWTLWYCO LGAAGTTER 1 LYGPGGSSN GGGGGGGGG GGGGGGGG ALFULOPPS 1 LYGPGGSLR GSGGGGGGGG GGGGGGGGGG GGGGGGGGGGGG  | scFv30 | 32   | <b>~</b> | ISCKASGETF TSYLFHWVRQ APGORLEWMG         | -   |
| 101   IRESEDEWGR GTLVTVSSGG GGSGGGSGG GGSDIQMTQS   151   RVTTTCRASE GIYWLAWYQ QKPCKAPKALL IYKAASALASG   151   VPFGSTLATISS LQPDDFATYY CQQYSNYPLIT FGGGTKLEIK   101   VTVSSGGGGS GGGSGGGGS ALSSELTQDP ATVYCARRRY   101   DYYKATWYQQ KPGQAPLLVF ESENRRPSGI PDRESGSNSG   151   DYYKATWYQQ KPGQAPLLVF ESENRRPSGI PDRESGSNSG   151   DYYKATWYQQ KPGQAPLLVF ESENRRPSGI PDRESGSNSG   101   QAEDBADYYC NSREIGTUNI LEGGGTKITV LGAAA   1 LVQPGGSLRL SCAAAGFTFS TERNWWRQA PGKGLEWVSY   101   GAEDBADYYC NSREIGTUNI LEGGGTKITV LGAAA   1 LVQPGGSLRL SCAAAGFTFS TERNWWRQA PGKGLEWVSY   101   GAEDBADYYC AAWDSLNGW VFGGGTKVTV   101   GAEDBADYYC AAWDSLNGW VFGGGTKVTV   101   CASSLAISGL QSEDEADYYC AAWDSLNGW VFGGTKVTV   101   VSSGGGSSS AFSWVRQAPG GGLQWMGGII PLFGAANYAQ   101   VSSGGGSGG GGSGGGGAQ SULTQLESAS GAPGQRTTY   101   VSSGGGSGG GGSGGGGAQ SULTQLESAS GAPGQRTTY   101   SSGLDWWGQC TLVTVSSGGG GSGGGGGG GSAQAVITQPP   101   SSGLDWWGQC TLVTVSSGGG GSGGGGGG GSAQAVITQP   101   SSGLDWWGQC TLVTVSSGGG GSGGGGGG GSAQAVITQP   101   SSGLDWWGQC TLVTVSSGGG GSGGGGGGG GSAQAVITQP   101   SSGLDWWGQC TLVTVSSGGG GSGGGGGG QSAQAVITQP   101   SGGTSSALAIS GLRSEDEADY YCAAWDDSLS GWVFGGGTK   101   GMDVWGRGT VTVSSGGG GSGGGGGG QSGGGGG QSAQAVITQP   101   GMDVWGRGT VTVSSGGG GGGGGGGG QGSGGGGG QGSGGGGG QGSGGGGG QGSGGGGG QGSGGGGG QGSGGGGG QGSGGGGG QGSGGGGG QGSGGGGG QGSGGGGGAQ QCTARRD YXCARGSGR   101   GMDVWGRGT VTVSSGGG GGGGGGGGG QGSGGGGG QGSGGGGG QGSGGGGGGGG   |        |      | 51       | LTGDTSTSTT YMELSSLTSE DTAVYYCARD         | 102 |
| 151 RVTITCRASE GIYHMIAWYQ QKPGKAPKLI IYKASSLASG 201 GTDETLISS LQPDDEATYY CQQYSNYPLT FGGGTKLEIK 101 VYVSSGGGS GGGSGGGGS ALSSELTQDP AVYYCARRYY 101 VYVSSGGGS GGGSGGGGS ALSSELTQDP AVYYCARRYY 101 VYVSSGGGS GGGSGGGGS ALSSELTQDP AVYYCARRYY 101 QAEDDEADYYC NSREIGTNRI LEGGGTKLTV LGAAA 1 LVQPGGSLRL SCAAAGFTES TEENNWYRQA PGKGLEWVSY 51 ADSVKGRFTI SRDNANNSLY LQMNSLTAED TAVYYCAREK 101 GMDVWGRGTT VTVSSGGGS GGGSGGGGS ALPVLTQPPS 151 ISCSGSSNI GSWTLNWYQQ LRCTAPKLLI YSNDQRPSGV 201 TSASIAISGL QSEDEADYYC AANDDSLINGW VEGGGTKVYV 201 TSASIAISGL QSEDEADYYC AANDDSLINGW VEGGGTKVYV 201 TSASIAISGL QSEDEADYYC AANDDSLINGW VEGGGTKVYV 101 VSSGGGSGG GGSGGGSA SUFQLPSGS GAPGQRITIS 151 WYVDWYQUY B GTARKLEIY ROWNDSLING RSPGTYYGM 101 VSGGGSGGGG GSGGGGSA SULTQLPSA GAPGGRITIS 152 BDEADYYCLT WDDSLSGPVE GGGTKLTVIG AAA 1 ACKGFGYTEV DHGISWVRQA PGGGLEMWGM INTHDGHTNY 51 TTDASINTSY MELRSLTSDD TAVYYCARGE GTRTAHRSRR 101 SGTSASLAIS GLRSEDEADY YCAANDDSLS GWRGGTKLIV 102 SGTSASLAIS GLRSEDEADY YCAANDDSLS GWRGGTKLIV 103 SGTSASLAIS GLRSEDEADY YCAANDDSLS GWRGGTKLIV 104 SGTSASLAIS GLRSEDEADY YCAANDDSLS GWRGGTKVY 105 GGGSGGGG GGGGGGGGGGGGGGGGGGGGGGGGGGGG   |        |      | 101      | GTLVTVSSGG GGSGGGGSGG GGSDIQMTQS         | 707 |
| 201 GTDFTLTISS LQPDDFATYY CQQYSNYPLT EGGGTKLEIK  1 VRPGGSIRLS CAASGFTEDD YGMSWYRQAP GKGLEWVSGI  101 VTVSSGGGG GGGGGGGG ALSSELTQDP ATVYCARRRY  101 VTVSSGGGG GGGGGGGG ALSSELTQDP ATVYCARRRY  101 DKYTATWYQQ KPGQAPLLVF ESBNRRPSGI PDRFSGSNSG  201 DAVYGRGRFTI SRDNANNSLY LQMNSLTAED TAVYYCAREK  101 GMDVWGRGTT VTVSSGGGG GGGGGGGGS ALPVLTQPPS  151 ISCSGSSNI GSNTLNWYQQ LPGTAPKLLI YSNDQRPSGV  201 TSASIAISGL QSEDBADYYC AAWDDSLNGW VEGGTKVTV  101 SASIGGTSSS AFSWYRQAPG GGGGGGGGS ALPVLTQPPS  101 SASIGGTSSS AFSWYRQAPG GGGGGGGG ALPVLTQPPS  101 SASIGGTSSS AFSWYRQAPG GGGGGGGGG ALPVLTQPPS  202 DESTGSYMK LENLQSDDTA VYCCATNGQT RSPPGYYCGM  103 SGGLDVWGQG GGGGGGGSAQ SVLTQLPPSAS GAPGGRITIS  204 BASGGTSSS AFSWYRQAPG GGGGGGGGG GAPGANTTOP  105 SGGLDVWGQG TLVTVSSGGG GSGGGGGGG GSAQAVLTQP  206 SGGGGGGG GGGGGGGGG GSAQAVLTQP  207 SGGGGGGG GGGGGGGGG GSAQAVLTQP  208 SGGTKATY WDDSLSGPVE GGTKLTVLQP  208 SGGGGGGGG GSGGGGGGG GSAQAVLTQP  209 SGGGGGGGG GSGGGGGGG GSAQAVLTQP  201 SGGGGGGGG TLVTVSSGG GSGGGGGGG GSAQAVLTQP  201 SGGGGGGG TLVTVSSGG GSGGGGGGG GSAQAVLTQP  202 SGGGGGGGG TLVTVSSGG GSGGGGGGG GSAQAVLTQP  203 SGGGGGGGG TLVTVSSGG GSGGGGGG GSAQAVLTQP  204 SGGGGGGGG TLVTVSSGG GSGGGGGGG GSAQAVLTQP  205 GGGGGGGGG GSGGGGGGGGGGGGGGGGGGGGGGGGG  |        |      | 151      | GIYHWLAWYQ QKPGKAPKLL IYKASSLASG         |     |
| 1 VRPGGSLRLS CAASGFTEDD YGMSWVRQAP GKGLEWVSGI     10   |        |      | 201      | LOPDDEATYY COOYSNYPLT FGGGTKLEIK         |     |
| 101   VTVSSGGGGS GGGSGGGGS ALSSELTQDP ATVSVALGQT   101   VTVSSGGGGS GGGSGGGGS ALSSELTQDP ATVSVALGQT   151   DKYYATWYQQ KPGQAPILLYF ESENRRPSGI PDRESGSNSG   201   QAEDEADYYC NSREIGTNRI LEGGGTKLTV LGAAA   LVQPGGSLRL SCAAAGFTES TFEMNWYRQA PGKGLEWVSY   201   LVQPGGSLRL SCAAAGFTES TFEMNWYRQA PGKGLEWVSY   201   TGASLAISGL GSNTLNWYQQ LPGTAPKLLI YSNDQRRSGV   201   TGASLAISGL GSNTLNWYQAPG GGLQWMGGII PLEGAANYAQ   201   DESTGTSYMK LENLQSDDTA VYFCATNGQT RSPGYYYGM   101   VSSGGGGSGG GGSGGGSAQ SVLTQLPSAS GAPGQRITIS   101   VSSGGGGSGG GGSGGGSAQ SVLTQLPSAS GAPGQRITIS   101   SGCLDVWGQ TLVTVSSGG GSCGGGGG GSAQAVITQP   101   SGCLDVWGQ TLVTVSSGGG GSCGGGGG GSAQAVITQP   101   SGCLDVWGG TLVTVSSGGG GSCGGGGG GSAQAVITQP   101   SGCLSVSCT STSTVYMEL SINRSDDSLS GWVGGGTKL V STSTVYMEL SINRSDDSLS GWVGGGTK V STSTVYMEL SINRSDDSLS GVVGGGGGG RQSVLTQPPS   151   SCCSGSGGGG GGSGGGGG GSCGGGG AQSVLTQPPS   151   SCCSSSSNV GSNVSWYQQ FCTAPRKLLI YRNNQRSGV   151   SCCSSSSNV GSNVSWYQQ FCTAPRKLLI YRNNQRSGV   151   SCCSSSSNV GSNVSWYQQ FCTAPRKLLI YRNNQRSGV   151   SCCSSSSNV GSNVSWYQQ FCTAPRKLLI YRNNQRSGY   151   SCCSSSSNV GSNVSWYQQ FCTAPRKLLI YRNNQRSGY   151   SCCSSSSNV GSNVSWYQQ FCTAPRKLLI YRNNGRSGY   151   SCCSSSSNV GSNVSWYQQ FCTAPRKLI YRNNGRSGY   151   SCCSSSSNV GSNVSWSWYQQ FCTAPRESGGS   151   SCCSSSSNV GSNVSWSWYQQ FCTAPRESGGG SQCGGGGG SQCGGGGG SQCGGGG SQCGGGGG GGGGGGG   151   15 | scFv31 | 33   | 1        | CAASGETEDD YGMSWVRQAP GKGLEWVSGI         |     |
| 101 VTVSSGGGS GGGSGGGGS ALSSELTQDP 151 DKYYATWYQQ KPGQAPLLVF FSENRRPSGI 201 QAEDEADYYC NSREIGTNRI LFGGGTKLTV 51 LVQPGGSLRL SCAAAGFTES TFEMNWVRQA 51 ADSVKGRFTI SRDNANNSLY LQMNSLTAED 101 GMDVWGRGTT VTVSSGGGG GGGGSGGGS 151 ISCSGSSNI GSNTLNWYQQ LPGTAPKLLI 201 TSASLAISGL QSEDEADYYC AAWDDSLNGW 51 RASGGTSSS AFSWVRQAPG QGLQWMGGTI 101 VSSGGGGGG GGSGGGGSQ SVLTQLPSAS 151 NYVDWYKQLP GTAPKLETYK NDQRPSGVPG 201 EDEADYYCLT WDDSLSGPVF GGGTKLTVLG 201 EDEADYYCLT WDDSLSGPVF GGGTKLTVLG 201 EDEADYYCLT WDSSLSGPVF GGGTKLTVLG 201 EDEADYYCLT WDSSLSGPVF GGGTKLTVLG 201 EDEADYYCLT WDSSLSGPVF GGGTKLTVLG 201 SGGSGGGGG TLVTVSSGG GSGGGGGG 151 VTISCSGSSS NIGSNVYWY QQLPGTAPKL 201 SGTSASLAIS GLRSEDEADY YCAAWDDSLS 101 GMDVWGRGTL VTVSSGGG GGGSGGGS 151 ISCSGSSSNV GSNVSWYQQ FPGTAPKLLI 201 ISASLAISGL RSEDEADFYC VAWDDSLREY   |        |      | 51       | RDNAKNSLYL QINSLRAEDT AVYYCARRRY         | 103 |
| 151   DKYYATWYQQ KPGQAPLLVF FSENRRPSGI PDRFSGSNSG     201   QAEDEADYYC NSREIGTNRI LEGGGTKLTV LGAAA     1   LVQPGGSLRL SCAAAGFTES TFEMNWYRQA PGKGLEWVSY     21   ADSVKGRFTI STDNANNSLY LQMNSLTAED TAVYYCAREK     101   GMDVWGRGTT VTVSSGGGS GGGGSGGGS ALPVLTQPPS     151   ISCSGSSNI GSNTLNWYQQ LPGTAPKLLI YSNDQRPSGV     1   TASGGTSSS AFSWYRQAPG GGLQWMGGTI PLFGAANYAQ     1   LVSGGGGSG GGGGGSAQ SVLTQLPSAS GAPGGTKYYGM     101   VSSGGGGSG GGGGGSAQ SVLTQLPSAS GAPGGRTTS     101   STGTTSYMK LENLQSDTA YYCARGG ETKTAHRSRR     101   STGTTSYMY MDDSLSGPVF GGGTKLTVLC AAA     102   STGTTSYNYWYQ QQLFGTAPKL LIYRNNQRPS     103   STGTSASLAIS GIRSEDEADY YCARGGGTKL     104   STGTTSTSTYNYWY QQLFGTAPKL LIYRNNQRPS     106   STGTTSTSTYNYWY QQLFGTAPKL LIYRNNQRPS     107   STGTSASLAIS GIRSEDEADY YCARGGGTKL     108   STGTSASLAIS GIRSEDEADY YCARGGGTKL     109   GMDVWGRGT VTVSSGGG GGGGGGGG GSAQAVLTQP     101   GMDVWGRGT VTVSSGGG GGGGGGGG AQSVLTQPPS     101   GMDVWGRGT VTVSSGGG GGGGGGGGG AQSVLTQPPS     101   GMDVWGRGT VTVSSGGG GGGGGGGGG AQSVLTQPPS     101   GMDVWGRGT VTVSSGGG GGGGGGGGG AQSVLTQPPS     101   GMDVWGRGT VTVSSGGG GGGGGGGGGGGGGGGGGGGGGGGGGGGG  |        |      | 101      | GGGGSGGGS ALSSELTODP                     | 101 |
| 201 QAEDEADYYC NSREIGTNRI LEGGGTKITV LGAAA  1 LVQPGGSLRL SCAAGFTES TFEMNWVRQA PGKGLEWVSY 51 ADSVKGRFTI SRDNANNSLY LQMNSLTAED TAVYYCAREK 101 GMDVWGRGTT VTVSSGGGS GGGGGGGS ALPVLTQPPS 151 ISCSGSSNI GSNTLNWYQQ LPGTAPKLLI YSNDQRPSGV 201 TSASLAISGL QSEDEADYYC AAWDDSLNGW VEGGGTKVTV 1 RASGGTSSSS AFSWVRQAPG QGLQWMGGII PLEGAANYAQ 51 DESTGTSYMK LENLQSDDTA VYFCATNGQT RSPPGYYYGM 101 VSSGGGSGG GGSGGGSAQ SVLTQLPSAS GAPGQRITIS 151 NYVDWYKQLP GTAPKLETYK NDQRPSGVPG RESGSKSGTS 201 EDEADYYCLT WDDSLSGPVF GGGTKLTVLG AAA 1 ACKGFGYTEV DHGISWVRQA PGQGLEWMGW INTHDGHTNY 51 TTDASINTSY MELRSLTSDD TAVYYCARGG GSRQAVLTQP 151 VTISCSGSSS NIGSNYVWY QQLPGTAPKL LIYRNNQRPS 201 SGTSASLAIS GLRSEDEADY YCAAWDDSLS GWVEGGTKL 101 SGGRVTMTRD TSTSTVYMEL SSLRSEDTAV YYCARGSGAR 101 GMDVWGRGTL VTVSSGGGS GGGGGGGS AQSVLTQPPS 151 ISCSGSSSNV GSNYVSWYQQ PGGTAPKLLI YRNNQRPSGV 201 ISASLAISGL RSEDEADFYC VAWDDSLREY VEGTKVTV  |        |      | 151      | KPGQAPLLVF FSENRRPSGI PDRFSGSNSG         |     |
| 1 LVQPGGSLRL SCAAAGFTES TFEMNWVRQA PGKGLEWVSY 51 ADSVKGRFTI SRDNANNSLY LQMNSLTAED TAVYYCAREK 101 GMDVWGRGTT VTVSSGGGS GGGSGGGGS ALPVLTQPPS 151 ISCSGSSSNI GSNTLNWYQQ LPGTAPKLLI YSNDQRPSGV 201 TSASLAISGL QSEDEADYYC AAWDDSLNGW VFGGTKVTV 51 RASGGTSSSS AFSWVRQAPG QGLQWMGGII PLFGAANYAQ 101 VSSGGGSGG GGSGGGGSAQ SVLTQLPSAS GAPGQRITIS 151 NYVDWYKQLP GTAPKLFIYK NDQRPSGVPG RFSGSKSGTS 201 EDEADYYCLT WDDSLSGPVF GGGTKLTVLG AAA 1 ACKGFGYTFV DHGISWVRQA PGQGLEWMGW INTHDGHTNY 51 TTDASINTSY MELRSLTSDD TAVYYCARGG GSAQAVLTQP 151 VTISCSGSSS NIGSNYVWY QQLPGTAPKL LIYRNNQRPS 201 SGTSASLAIS GLRSEDEADY YCAAWDDSLS GWVFGGGTKL 201 SGTSASLAIS GLRSEDEADY YCAAWDDSLS GWVFGGGTKL 201 GMDVWGRGTL VTVSSGGG GGGGGGGG AQSVLTQPPS 151 FQGRVTMTRD TSTSTVYMEL SSLRSEDTAV YYCARGSGAR 101 GMDVWGRGTL VTVSSGGGS GGGGGGGGS AQSVLTQPPS 151 ISCSGSSSNV GSNYVSWYQQ FPGTAPKLLI YRNNQRPSGV 201 ISASLAISGL RSEDEADFYC VAWDDSLREY VFGTGTKVTV   |        |      | 201      | NSREIGTNRI LEGGGTKLTV                    |     |
| 101   GMDVWGRGTT VTVSSGGGS GGGSGGGGS ALPVLTQPPS   151   ISCSGSSNI GSNTLNWYQQ LPGTAPKLLI YSNDQRPSGV   201   TSASLAISGL QSEDEADYYC AAWDDSINGW VFGGTKVTV   201   TSASLAISGL QSEDEADYYC AAWDDSINGW VFGGTKVTV   201   TSASCGTSSS AFSWVRQAFG QGLQWMGGII PLFGAANYAQ   1   | scFv32 | - 34 | τ        | SCAAAGETES TEEMNWVRQA PGKGLEWVSY         |     |
| 101 GMDVWGRGTT VTVSSGGGS GGGSGGGGS ALPVLTQPPS 151 ISCSGSSSNI GSNTLNWYQQ LPGTAPKLLI YSNDQRPSGV 201 TSASLAISGL QSEDEADYYC AAWDDSLNGW VFGGGTKVTV 201 RASGGTSSS AFSWVRQAPG QGLQWMGGII PLFGAANYAQ 101 VSSGGGSGG GGSGGGGAQ SVLTQLPSAS GAPGQRITIS 101 VSSGGGSGG GGSGGGGSAQ SVLTQLPSAS GAPGQRITIS 201 BDEADYYCLT WDDSLSGPVF GGGTKLTVLG AAA 201 BDEADYYCLT WDDSLSGPVF GGGTKLTVLG AAA 201 ACKGFGYTFV DHGISWVRQA FGQGLEWMGW INTHDGHTNY 51 TTDASINTSY MELRSLTSDD TAVYYCARGG ETRTAHRSRR 101 SSGLDVWGQG TLVTVSSGGG GSGGGSGGG GSAQAVLTQP 151 VTISCSGSSS NIGSNYVWY QQLPGTAPKL LIYRNNQRPS 201 SGTSASLAIS GLRSEDEADY YCAAWDDSLS GWVFGGGTKL 37 I PGASVKVSCK ASGYTFTSYY MHWVRQAPGQ GLEWMGIINP 51 EQGRVTMTRD TSTSTVYMEL SSLRSEDTAV YYCARGSGAR 101 GMDVWGRGTL VTVSSGGGS GGGGSGGGS AQSVLTQPPS 151 ISCSGSSSNV GSNYVSWYQQ FPGTAPKLLI YRNNQRPSGV   |        |      | 51       | SRDNANNSLY LOMNSLTAED TAVYYCAREK         | 104 |
| 151 ISCSGSSSNI GSNTLNWYQQ LPGTAPKILI YSNDQRPSGV 201 TSASLAISGL QSEDEADYYC AAWDDSLNGW VEGGTKVTV 51 RASGGTSSS AFSWVRQAPG QGLQWMGGII PLFGAANYAQ 51 DESTGTSYMK LENLQSDDTA VYFCATNGQT RSPPGYYYGM 101 VSSGGGSGG GGSGGGSAQ SVLTQLPSAS GAPGQRITIS 151 NYVDWYKQLP GTAPKLFIYK NDQRPSGVPG RESGSKSGTS 201 EDEADYYCLT WDDSLSGPVF GGGTKLTVLG AAA 1 ACKGFGYTFV DHGISWVRQA PGQLEWMGW INTHDGHTNY 51 TTDASINTSY MELRSLTSDD TAVYYCARGG ETRTAHRSRR 101 SSGLDVWGQG TLVTVSSGGG GSGGGGSGG GSAQAVLTQP 151 STASSLAIS GIRSEDEADY YCAAWDDSLS GWVFGGGTKL 201 GADSVKVSCK ASGYTFTSYY MHWVRQAPG GLEWMGIINP 51 FQGRVTWTRD TSTSTVYMEL SSLRSEDTAV YYCARGSGAR 101 GMDVWGRGTL VTVSSGGGS GGGSGGGS AQSVLTQPPS 151 ISCSGSSSNV GSNYVSWYQQ FPGTAPKILI YRNNQRPSGV 201 ISASLAISGL RSEDEADFYC VAWDDSLREY VFGTGKVTV   |        |      | 101      | VIVSSGGGG GGGGGGGG ALPVLTQPPS            | 101 |
| 201 TSASLAISGL QSEDEADLYC AAWDDSLNGW VEGGGTKVTV  35 1 RASGGTSSS AFSWVRQAPG QGLQWMGGII PLEGAANYAQ 51 DESTGTSYMK LENLQSDDTA VYFCATNGQT RSPPGYYGM 101 VSSGGGSGG GGSGGGSAQ SVLTQLPSAS GAPGQRITIS 151 NYVDWYKQLP GTAPKLEIYK NDQRPSGVPG RESGSKSGTS 201 EDEADLYCLT WDDSLSGPVF GGGTKLTVLG AAA  56 1 ACKGFGYTFV DHGISWVRQA PGGLEWMGW INTHDGHTNY 51 TTDASINTSY MELRSLTSDD TAVYYCARGG ETRTAHRSRR 101 SSGLDVWGQG TLVTVSSGGG GSGGGGSGG GSAQAVLTQP 151 VTISCSGSS NIGSNYVWY QQLPGTAPKL LIYRNNQRPS 201 SGTSASLAIS GLRSEDEADLY YCAAWDDSLS GWVFGGGTKL 201 GMDVWGRGTL VTVSSGGGS GGGGSGGG GSQQVLTQPPS 101 GMDVWGRGTL VTVSSGGGS GGGSGGGGS AQSVLTQPPS 151 ISCSGSSSNV GSNYVSWYQQ FPGTAPKLLI YRNNQRPSGV 201 ISASLAISGL RSEDEADFYC VAWDDSLREY VFGTGKVTV   |        |      | 151      | GSNTLNWYQQ LPGTAPKLLI YSNDQRPSGV         |     |
| 1 RASGGTSSSS AFSWVRQAPG QGLQWMGGII PLEGAANYAQ 51 DESTGTSYMK LENLQSDDTA VYECATNGQT RSPPGYYGM 101 VSSGGGGSG GGSGGGSAQ SVLTQLPSAS GAPGQRITIS 151 NYVDWYKQLP GTAPKLFIYK NDQRPSGVPG RESGSKSGTS 201 EDEADYYCLT WDDSLSGPVF GGGTKLTVLG AAA 51 ACKGFGYTEV DHGISWVRQA PGQGLEWMGW INTHDGHTNY 51 TTDASINTSY MELRSLTSDD TAVYYCARGG ETRTAHRSRR 101 SSGLDVWGQG TLVTVSSGGG GSGGGGSGG GSAQAVLTQP 151 VTISCSGSSS NIGSNYVYWY QQLPGTAPKL LIYRNNQRPS 201 SGTSASLAIS GLRSEDEADY YCAAWDDSLS GWVFGGGTKL 202 SGTSASLAIS GLRSEDEADY YCAAWDDSLS GWVFGGGTKL 203 GMDVWGRGTL VTVSSGGGS GGGGSGGGS AQSVLTQPPS 101 GMDVWGRGTL VTVSSGGGS GGGSGGGGS AQSVLTQPPS 151 ISCSGSSSNV GSNYVSWYQQ FPGTAPKILI YRNNQRPSGV  |        |      | 201      | QSEDEADYYC AAWDDSLNGW VFGGGTKVTV         |     |
| 101 VSSGGGSGG GGSGGGSAQ SVLTQLPSAS GAPGGRITIS 1151 NYVDWYKQLP GTAPKLEIYK NDQRPSGVPG RESGSKSGTS 201 EDEADYYCLT WDDSLSGPVF GGGTKLTVLG AAA  36 1 ACKGFGYTFV DHGISWVRQA PGQGLEWMGW INTHDGHTNY 51 TTDASINTSY MELRSLTSDD TAVYYCARGG ETRTAHRSRR 101 SSGLDVWGQG TLVTVSSGG GSGGGGSGG GSAQAVLTQP 151 VTISCSGSSS NIGSNYYWY QQLPGTAPKL LIYRNNQRPS 201 SGTSASLAIS GLRSEDEADY YCAAWDDSLS GWVEGGGTKL 37 1 PGASVKVSCK ASGYTETSYY MHWVRQAPGQ GLEWMGIINP 51 FQGRVTMTRD TSTSTVYMEL SSLRSEDTAV YYCARGSGAR 101 GMDVWGRGTL VTVSSGGGS GGGSGGGGS AQSVLTQPPS 151 ISCSGSSSNV GSNYVSWYQQ FPGTAPKLLI YRNNQRPSGV 201 ISASLAISGL RSEDEADFYC VAWDDSLREY VEGTGKVTV   | scFv33 | 35   | 7        | AFSWVRQAPG QGLQWMGGII PLFGAANYAQ         |     |
| 101 VSSGGGSGG GGSGGGSAQ SVLTQLPSAS GAPGQRITIS 151 NYVDWYKQLP GTAPKLFIYK NDQRPSGVPG RESGSKSGTS 201 EDEADYYCLT WDDSLSGPVF GGGTKLTVLG AAA  36 1 ACKGFGYTFV DHGISWVRQA PGQGLEWMGW INTHDGHTNY 51 TTDASINTSY MELRSLTSDD TAVYYCARGG ETRTAHRSRR 101 SSGLDVWGQG TLVTVSSGG GSGGGGSGG GSAQAVLTQP 151 VTISCSGSSS NIGSNYVYWY QQLPGTAPKL LIYRNNQRPS 201 SGTSASLAIS GLRSEDEADY YCAAWDDSLS GWVEGGGTKL 201 SGTSASLAIS GLRSEDEADY YCAAWGDDSLS GWVEGGGTKL 51 PGASVKVSCK ASGYTETSYY MHWVRQAPGQ GLEWMGIINP 51 GMDVWGRGTL VTVSSGGGS GGGSGGGGS AQSVLTQPPS 101 GMDVWGRGTL VTVSSGGGS GGGSGGGGS AQSVLTQPPS 151 ISCSGSSSNV GSNYVSWYQQ FPGTAPKLLI YRNNQRPSGV 201 ISASLAISGL RSEDEADFYC VAWDDSLREY VEGTGKVTV  |        |      | 51       | LENLQSDDTA VYFCATNGQT RSPPGYYYGM         | 105 |
| 151 NYVDWYKQLP GTAPKLFIYK NDQRPSGVPG RESGSKSGTS 201 EDEADYYCLT WDDSLSGPVF GGGTKLTVLG AAA  36 1 ACKGFGYTEV DHGISWVRQA PGQGLEWMGW INTHDGHTNY 51 TTDASINTSY MELRSLTSDD TAVYYCARGG ETRTAHRSRR 101 SSGLDWGQG TLVTVSSGGG GSGGGSGGG GSAQAVLTQP 151 VTISCSGSSS NIGSNYVYWY QQLPGTAPKL LIYRNNQRPS 201 SGTSASLAIS GLRSEDEADY YCAAWDDSLS GWVEGGGTKL 37 1 PGASVKVSCK ASGYTETSYY MHWVRQAPGQ GLEWMGIINP 51 EQGRVTWTRD TSTSTVYMEL SSLRSEDTAV YYCARGSGAR 101 GMDVWGRGTL VTVSSGGGS GGGSGGGGS AQSVLTQPPS 151 ISCSGSSSNV GSNYVSWYQQ FPGTAPKLLI YRNNQRPSGV 201 ISASLAISGL RSEDEADFYC VAWDDSLREY VEGTGTKVTV  |        |      | 101      | GGSGGGSAQ SVLTQLPSAS GAPGQRITIS          | 3   |
| 36 1 EDEADYYCLT WDDSLSGPVF GGGTKLTVLG AAA  1 ACKGFGYTEV DHGISWVRQA PGQGLEWMGW INTHDGHTNY 51 TTDASINTSY MELRSLTSDD TAVYYCARGG ETRTAHRSRR 101 SSGLDWGQG TLVTVSSGGG GSGGGSGGG GSAQAVLTQP 151 VTISCSGSS NIGSNYYWY QQLPGTAPRL LIYRNNQRPS 201 SGTSASLAIS GLRSEDEADY YCAAWDDSLS GWVFGGGTKL 37 1 PGASVKVSCK ASGYTETSYY MHWVRQAPGQ GLEWMGIINP 51 FQGRVTMTRD TSTSTVYMEL SSLRSEDTAV YYCARGSGAR 101 GMDVWGRGTL VTVSSGGGS GGGGSGGGS AQSVLTQPPS 151 ISCSGSSSNV GSNYVSWYQQ FPGTAPKILI YRNNQRPSGV  |        |      | 151      | GTAPKLFIYK NDQRPSGVPG RFSGSKSGTS         |     |
| 1 ACKGEGYTEV DHGISWVRQA PGQGLEWMGW INTHDGHTNY 51 TTDASINTSY MELRSLTSDD TAVYYCARGG ETRTAHRSRR 101 SSGLDVWGQG TLVTVSSGGG GSGCGCSGGG GSAQAVLTQP 151 VTISCSGSS NIGSNYVWY QQLPGTAPKL LIYRNNQRPS 201 SGTSASLAIS GLRSEDEADY YCAAWDDSLS GWYFGGGTKL 201 PGASVKVSCK ASGYTETSYY MHWYRQAPGQ GLEWMGIINP 51 PGASVKYNTRD TSTSTVYMEL SSLRSEDTAV YYCARGSGAR 101 GMDVWGRGTL VTVSSGGGS GGGGSGGGS AQSVLTQPPS 151 ISCSGSSSNV GSNYVSWYQQ FPGTAPKILI YRNNQRPSGV 201 ISASLAISGL RSEDEADFYC VAWDDSLREY VFGTGTKVTV   |        |      | 201      | WDDSLSGPVF GGGTKLTVLG                    |     |
| 51 TTDASINTSY MELRSLTSDD TAVYYCARGG ETRTAHRSRR 101 SSGLDVWGQG TLVTVSSGGG GSGGGGGG GSAQAVLTQP 151 VTISCSGSSS NIGSNYVWY QQLPGTAPKL LIYRNNQRPS 201 SGTSASLAIS GLRSEDEADY YCAAWDDSLS GWYFGGGTKL 37 1 PGASVKVSCK ASGYTFTSYY MHWYQAPGQ GLEWMGIINP 51 FQGRVTMTRD TSTSTVYMEL SSLRSEDTAV YYCARGSGAR 101 GMDVWGRGTL VTVSSGGGS GGGGSGGGS AQSVLTQPPS 151 ISCSGSSSNV GSNYVSWYQQ FPGTAPKLLI YRNNQRPSGV 201 ISASLAISGL RSEDEADFYC VAWDDSLREY VFGTGTKVTV   | scFv34 | 36   |          | PGOGLEWMGW                               |     |
| 101 SSGLDVWGQG TLVTVSSGGG GSGGGGGGG GSAQAVLTQP 151 VTISCSGSSS NIGSNYVWY QQLPGTAPKL LIYRNNQRPS 201 SGTSASLAIS GLRSEDEADY YCAAWDDSLS GWVFGGGTKL  101 PGASVKVSCK ASGYTFTSYY MHWVRQAPGQ GLEWMGIINP 51 FQGRVTMTRD TSTSTVYMEL SSLRSEDTAV YYCARGSGAR 101 GMDVWGRGTL VTVSSGGGGS GGGGSGGGS AQSVLTQPPS 151 ISCSGSSSNV GSNYVSWYQQ FPGTAPKLLI YRNNQRPSGV 201 ISASLAISGL RSEDEADFYC VAWDDSLREY VFGTGTKVTV   |        |      | 51       | MELRSLTSDD TAVYYCARGG ETRTAHRSRR         | 106 |
| 151 VTISCSGSSS NIGSNYVYWY QQLPGTAPKL LIYRNNQRPS 201 SGTSASLAIS GLRSEDEADY YCAAWDDSLS GWVEGGGTKL  101 PGASVKVSCK ASGYTFTSYY MHWVRQAPGQ GLEWMGIINP 51 FQGRVTMTRD TSTSTVYMEL SSLRSEDTAV YYCARGSGAR 101 GMDVWGRGTL VTVSSGGGGS GGGGSGGGGS AQSVLTQPPS 151 ISCSGSSSNV GSNYVSWYQQ FPGTAPKLLI YRNNQRPSGV 201 ISASLAISGL RSEDEADFYC VAWDDSLREY VFGTGTKVTV  |        |      | 101      | TLVTVSSGGG GSGGGGGGG GSAQAVLTQP          |     |
| 37 1 SGTSASLAIS GLRSEDEADY YCAAWDDSLS GWVFGGGTKL  1 PGASVKVSCK ASGYTFTSYY MHWVRQAPGQ GLEWMGIINP 51 FQGRVTMTRD TSTSTVYMEL SSLRSEDTAV YYCARGSGAR 101 GMDVWGRGTL VTVSSGGGGS GGGGSGGGGS AQSVLTQPPS 151 ISCSGSSSNV GSNYVSWYQQ FPGTAPKLLI YRNNQRPSGV 201 ISASLAISGL RSEDEADFYC VAWDDSLREY VFGTGTKVTV   |        |      | 151      | NIGSNYVYWY QQLPGTAPKL LIYRNNQRPS         |     |
| 37 1 PGASVKVSCK ASGYTETSYY MHWVRQAPGQ GLEWMGIINP 51 FQGRVTMTRD TSTSTVYMEL SSLRSEDTAV YYCARGSGAR 101 GMDVWGRGTL VTVSSGGGGS GGGGSGGGGS AQSVLTQPPS 151 ISCSGSSSNV GSNYVSWYQQ FPGTAPKLLI YRNNQRPSGV 201 ISASLAISGL RSEDEADFYC VAWDDSLREY VEGTGTKVTV  |        |      | 201      | GLRSEDEADY YCAAWDDSLS GWVFGGGTKL         |     |
| 51 FQGRVTMTRD TSTSTVYMEL SSLRSEDTAV YYCARGSGAR 101 GMDVWGRGTL VTVSSGGGS GGGSGGGGS AQSVLTQPPS 151 ISCSGSSSNV GSNYVSWYQQ FPGTAPKLLI YRNNQRPSGV 201 ISASLAISGL RSEDEADFYC VAWDDSLREY VFGTGTKVTV   | scFv35 | 37   | 1        | ASGYTETSYY MHWVRQAPGO GLEWMGIINP         |     |
| GMDVWGRGTL VTVSSGGGGS GGGGSGGGGS AQSVLTQPPS<br>ISCSGSSSNV GSNYVSWYQQ FPGTAPKLLI YRNNQRPSGV<br>ISASLAISGL RSEDEADFYC VAWDDSLREY VFGTGTKVTV  |        |      | 51       | TSTSTVYMEL SSLRSEDTAV YYCARGSGAR         | 107 |
| ISCSGSSSNV GSNYVSWYQQ FPGTAPKLLI YRNNQRPSGV<br>ISASLAISGL RSEDEADFYC VAWDDSLREY VFGTGTKVTV   |        |      | 101      | VTVSSGGGGS GGGSGGGGS AQSVLTQPPS          | 701 |
| ISASLAISGL RSEDEADFYC VAWDDSLREY VFGTGTKVTV  |        |      | 151      | GSNYVSWYQQ FPGTAPKLLI YRNNQRPSGV         |     |
|  |        |      | 201      |  |     |

F19. 10

|  | 108  | 100   |  |   |
|--|--|---|--|---|
| ESGGGLVQPG GSLRLSCAAS GFTFSSYAMS WVRQAPGKGL EWVSAISGSG | GSTYYADSVK GRFTISRDNS KNTLYLQMNS LRAEDTAVYY CAKGGTRVTH | RGGFDIWGRG TMVTVSSGGG GSGGGGGGGGGGGTPVLTQP PSASGAPGQR | ITISCSGSTF NIGRNYVDWY KQLPGTAPKL FIYKNDQRPS GVPDRFSGSK | SGTSASLVVS GLRSEDEADY YCLTWDDSLS GPVFGGGTKL TVLGAAA |
|  | 51   | 101   | 151  | 201   |
| 38   |  |   |  |   |
| scFv36   |  |   |  |   |

| Ref.: | SEQ ID No. | Nucle | ucleotide Sequence  |
|-------|------------|-------|---|
| scFv1 | r          |       | GAGGTCCAGCTGCAACAGTCTGGACCTGGTGAAGCCTGGGGCTTTAGTGAAGATATCCTGCAAGG         |
|       | `          | 71    | CCTCGGGATACACCGTCACAAGCTACGATATAAACTGGGTGAAGCAGAGGCCTGGACAGGGGACTTGAGTG   |
| ·     |            | 141   | GATTGGATGGATTTATCCTGGAGATGGTACTAAGTACAATGAGAAATTCAAGGGCAAGGCCACACTG       |
|       |            | 211   | ACTGTAGACAAATCCTCCACCACAGTCTACATGCAGCTCAGCAGCCTGACTTCTGAGAACTCTGCAGTCT    |
|       | -          | 281   | ATTTCTGTGCAAGAGGTGGTAAATACTTTGACTACTGGGGCCCAAGGCACCACTCTCACAGTGTCGACAGG   |
|       |            | 351   | TGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGAAGTGCACTCGACATTGTGATGACACAGTCT    |
|       |            | 421   | CCAAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCGTCACCTGCAAGGCCAGTCAGAATGTGGCTA    |
|       |            | 491   | CTAATGTAGCCTGGTATCAACAGAAACCAGGGCAATCTCCTAAACCACTGACTTACTCGGCATCCTTCCG    |
|       |            | 561   | GICCAGIGGAGICCCIGAICGCIICACAGGCAGIGGAICIGGGACAGAIIITCACICICACCAICAGCAAI   |
|       |            | 631   | GIGCAGICTGAAGACTIGGCAGAGTATTTCTGTCAGCAATATAACAGCTATCCGTACACGTTCGGAGGGG    |
|       |            | 701   | GGACCAAGCTGGAAATAAAAGCGGCCGCAGGTGCGCCGGTGCCGTATCCAGATCCGCTGGAACCGCGTGG    |
|       |            | 771   | GCCCCCAAGCCCTTGGAGCCACCTCGAAAATAA   |
| scFv2 | 4          | 1     | GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCTTGTGCAG    |
|       | ,          | 71    | CCTCTGGATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTG    |
|       |            | 141   | GGTCTCAGCTATTAGTGGTAGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATC       |
|       |            | 211   | TCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGT    |
|       |            | 281   | ATTACTGTGCGCGAGACTCGGGGCTACAGCAGGGACCCCGCCGAAAGAGGGGGCCCGAGTAAATTTCTCCTA  |
|       |            | 351   | CTACGGTCTGGACGTCTGGGGGGGGGGGGACCACGGTCACCGTCTCGAGTGGAGGCGGCGGTTCAGGCGGA   |
|       |            | 421   | GGTGGCTCTGGCGGTGGCGGAAGTGCACAGGCTGTGCTGACTCAGCGTCCTCAGCGTCTGGGACCCCCG     |
|       |            | 491   | GGCAGAGGGTCACCATCTCTTGTTCTGGAAGCAACTCCAACATCGGACGCAATTATGTATTCTGGTACCA    |
|       |            | 261   | GCAGTICCCAGGAACGGCCCCCAAAAICCICAICIACAGGAACAAICAGCGGCCCICAGGGGTCCCIGAC    |
|       |            | 631   | CGATICICTGGCICCAAGTCTGGCACATCAGCCTCCCTGGCCATGAGTGGGCCTCCGGTCCGAGGATGAGG   |
|       |            | 701   | CTGATTATTACTGTGCATCATGGGATGACAGCCTGACTTGGGTGTTCGGCGGAGGGACCAAGGTCACCGT    |
|       |            | 771   | CCTAGGTGCGGCCGCAGGTGCGCGGTGCCGTATCCAGATCCGCTGGAACCGCGTGGGGGCCGCAAGCGCT    |
|       |            | 841   | TGGAGCCACCGCAGTTCGAAAATAA   |
| scFv3 | 39         | τ     | GGGCCTCAGTGAAGGTCTCCTGCAAGACCTCTGGATACACCTTCATCGCTATTATTATTCATTGGGTGCG    |
|       |            | 7.1   | ACAGGCCCCTGGACAAGGGCTTGAGTGGATGGACGGATCAACCCTAACACTGGTGGCATAAACCTTGCA     |
|       |            | 141   | CAGAAGITICAGGGCAGGGTCACCGTGACCAGGGACACGTCCATCAGCACACACGCCCACATGGAGCTGAGTA |
|       |            | 211   | GGCTGAGCTCTGACGACACGGCCGTATACTACTGTGCGAGAGAGA                             |
|       |            | 281   | CCGTGGGATGGTGACTGCGGTTGGAATGGACGTCTGGGCCCGGGGAACCCTGGTCACCGTCTCGAGTGGA    |
|       |            | 351   | GGCGCCGGTTCAGGCGGAGGTGGCTGCGGGGAAGTGCACAGTCTGTCGTGACGCAGCCGCCCT           |
|       |            | 421   | CAATGTCTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTTCTGGGAGGAGGTCCAACATTGGAAGGAA    |
|       |            | 491   | TTATGTATACTGGTACCAGCAGTTCCCAGGAACGCCCCCCAAACTCCTCATTTATAGGAATAATGAACGG    |
|       |            | 561   | CCCTCAGGGGTCCCTGACCGATTCTCTGCCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGAC    |

F.0.4

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|       |      | 631   | TCCGGTCCGAGGGATGAGGCTGATTATTACTGCGCAACGTGGGATGACAGTCTGAGTGGGACTTGGGTGTTT  |
|-------|------|---|---|
| scFv4 | 40   | 21<br>141<br>211<br>281<br>351<br>421<br>491<br>561<br>631      | CTGTTGGAGTCTGGGGGGGGCTTGGTACGTCGCGGGGCTCCTGAGACTCTCCTGTGCAGCTCTGGAT  TCACCTTTAGCAGTCTGGGGGGGGCTTGGTACGTCCCTGGGGACGGCTCCTGTGCAGCTCTCAGGATGGGTTCTAGCAGTCTTGGGGGTTCTAGCAGTTGGGGGTTCTAGCAGTTGGTGGTTCTAGCAGTTGGTGGTTCTAGCAGTTGGTGGTTCTAGCAGTTGGTTTAGTTGCTTTAGTGGTTGTTTAGTGGTTGCTTTGCTTTGCTTTGCTTTGCTTTTAGTGGTTGGT  |
| scFv5 | . 41 | 71<br>141<br>281<br>281<br>351<br>421<br>491<br>561<br>631      | CAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTAGCAGCTTGGCAGGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGGGGTCTC AGCTATTAGTGGTAGTGGTAGCACATACTACGCCAGACTCCGTGAAGGGGCTGGAGGGGTCTC AGCTATTAGTGGTAGTGGTAGCACATACTACGCCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGA GACAATTCCAAGAACACGCTGTATTTGGGGGCTGGTTCGAGGCCGGGACCCTGGTATTACT GTGCGAGAGATTGGAGATGGCAACAATTGGGGGCTGGTTCGAGGGCCGAGGAACCCTGGTTATACT CTCACGCAGTTCCTGCTTCAGGTGGTGGTTCCAGGGGCAGACCCTCTTTTGGAGGCCAGTCCAGGTCTCTGTCTCTGTCTCCAGGGGCAGTCCAGGCCAGTTTTGG  TGCATCCACGCAGTGGCATTTTGCAGGTTCACTGGCAGTCCTCCAGGTCC ACCATCCACGCAAGGGCTGAGGATTTTGCAGTTATTACTGTCAGGCGTATGGTGCCAAGGGACAAGCTCCCAGATCA CCTTCGGCCAAGGGACACGAGTTAAACGTGCGCCCCC CCTTCGCCCAAGGGACACGAGTTAAACGTGCGCCCCCCCC |
| scFv6 | 42   | 1<br>71<br>141<br>211<br>281<br>351<br>421<br>421<br>491<br>631 | CAGCTGGTGCAGTCTGGGGGAGGCTTGGTGCAGCCGGGGGGTCCTGAGACTCGCCTGTGAAGCCTCTG GATTCAGGTTTAGCAGCTATGGCATGAGCTGGGTCCGCCAGGCAGG   |
| scFv7 | 43   | 71  | AAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCTGGAGGCACCTTCAGCAGTTATGCTATTA GTTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGAGGGATCATCCTATGCTGGTACACC  |

Fig. M

|        |          | 141    | AAACTACGCACAGAAGTTCCAGGACAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACATG  |
|--------|----------|--------|---|
|        |          | 211    | GAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGGGGGGGG               |
|        |          | 281    | TCGGTCGTGGCCCTTCGTACCACTACTACTACATGGACGTCTGGGGCAGGGGAACCCTGGTCACCGTCTC  |
|        |          | 351    | GAGTGGAGGCGCGCTTCAGGCGGAGGTGGCTCTGGCGGGGGGGG                            |
|        |          | 421    | CCGCCCTCAGCGTCTGGGACCCCCGGACAGGGTCACCATCTCTTGTTCTGGGGCCACCTCCAACATGG    |
|        |          | 44 Y L | GAAGGAAIIAIGIIIACIGGIACACACACACACCCCCAAGCICCICAICAIAGAAIGA              |
|        |          | 561    | TCAGCGTCCCTCAGGGGTCCCTGACCGATTCTCTGGGGTCCAAGTCTGGCACCTCAGCCTCCTGGCCATC  |
|        |          | 631    | AGTGGCCTCCGGTCCGACGATGAGGCTGATTATTACTGTGCTGCGTGGGACGACAACCTGAGTGGTCTAT  |
|        |          | 701    | TTTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTGCGGCCGC                             |
| scFv8  | 44       | -      | GCCCAGGTGCAGCTACAGCAGTGGGGCCCCAGGACTGGTGAAGGCTTCGGAGATCCTGTCCTCAACTGCA  |
| 2      | -        | 7.1    | CIGICICIGGIAGCICCCICAGCAGIGGIIACIACIACIGGAGCIGGAICCGCCAGCACCCAGGGAAGGG  |
|        |          | 141    | CCTGGAGTGGATTGGGTACATCCATTACAGTGGGAGCACGTACTACAACCCGTCCCTCAAGAGTCGAGTT  |
|        |          | 211    | ACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGCCGGGGCACACGG |
|        |          | 281    | CTGTGTATTATTGTGCGAGAGTTCCGTTGAGATTTGATGGTTTTGATGTCTGGGGCCAAGGCACCCTGGT  |
|        |          | 351    | CACCGTCTCGAGTGGTGGAGGCGGTTCAGGCGGAGGTGGCAGCGGCGGTGGCGGATCGGACATCCAGATG  |
|        |          | 421    | ACCCAGICICCTICCACCCIGICIGCAICIATIGGAGACAGAGICACCAICACCIGCCGGGCCAGIGAGG  |
|        |          | 491    | GTATTTATCACTGGTTGGCCTGGTATCAGCAGAAGCCAGGGAAAGCCCCTAAAACTCCTGATCTATAAGGC |
|        |          | 561    | CTCTAGTTTAGCCAGTGGGCCCCCATCAAGGTTCAGCGGCAGTGGGATCTGGGACAGATTTCACTCTCACC |
|        |          | 631    | ATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAATATAGTAATTATCCGCTCACTT  |
|        |          | 701    | TCGGCGGAGGGACCAAGCTGGAGATCAAACGTGCGGCCGC                                |
| scFv9  | 45       | -      | CTGAGCTGAAGAAGCCTGGGTCCTCGGTAAAGGTCTCCTGCAAGGCTCCTAGAGGCACCTTCAACAGTTA  |
|        | <u>.</u> | 71     | TGCTCTCAACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGGATGGGAGGGA               |
|        |          | 141    | GGTAGTGCAAATTACGCACCGAAGTTCCAGGGCAGAGTCACCATTACCGCGGACGAATCCACGACCACAC  |
|        |          | 211    | CCTACTIGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTATATTACTGTGCGCGAGCTCTCCATTT  |
|        |          | 281    | GGATTACGTTTGGAGGACTTATAATTACTACTTTGACAACTGGGGCAAAGGGACAATGGTCACCGTCTCG  |
|        |          | 351    | AGTGGAGGCGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGAAGTGCACTTTCTTCTGAGCTGACTC  |
|        |          | 421    | AGGACCCTGCTGTGTCTGTGGCCTTGGGACAGACAGTCAGGATCACATGCCAGGGAGACAGCCTCAGAAG  |
|        |          | 491    | TIATIATGCAAGCTGGTACCAGCAGAAGCCAGGACAGGCCCCTGTCCTTGTCATCTATGGTAAAAATAGT  |
|        |          | 561    | CGGCCCTCAGGGATCCCAGACCGATTCTCTGGCTCCGACTCAGGAAACACAGCTTCCTTGACCATCACTG  |
|        |          | 631    | GGGCTCAGGCGGAAGATGAGGCTGACTATTACTGTAACTCCCGGGACAGAAGTGGTAACCGCGTGGTCTT  |
| ¢      |          | 701    | CGCCGGAGGGACCAAGCTGACCGTCCTAGGTGCGCCCCC                                 |
| scFv10 | 46       |        | TCCCTGAGACTCTCCTGTGCGGCCTCTGGATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGG  |
|        |          | 71     | CTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCAGACTC  |
|        |          | 141    | CGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTG  |
|        |          | 211    | AGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGTTACGTATCACTATGACCATGACAGGCGTG  |
|        |          | 281    | GTGTGACCGCGCAAATATATAAACCACGGTTTGGACGTCTGGGGGGGG                        |

|        |    | 25.1 | ひしい かいまい まいまい かいかい ひかく かいかい かんかい かんかい かんしょう かいしゅん かいしゅん かいしゅん しゅうしゅう しゅう |
|--------|----|------|--|
|        |    | 421  | I GGAGGGCGGI I CAGGCGGGGGGGGCGCGCGGGGGGGGGG  |
|        |    | 491  | AGAATTATGTATACTGGTATCAGCAGCTCCCCAGGAACGCCCCCCAAACTCCTCTATAGGAATAATCA   |
|        |    | 561  | GCGGCCCTCAGGAGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGT   |
|        |    | 631  | GGGCTCCGGTCCGAGGATGAGGCTGATTATTATTGTGCGGCACGGGATAACGGCCTGAGTGCTTATGTGA   |
|        |    | 701  | TATTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTGCGGCCGC  |
| scFv11 | 47 | 1    | AGGTGAAAAAGCCCGGGGGAGTCTCTGAAGATCTCCTGCAAGGGTTCTGGATACAGCTTTCCCAACTACTG  |
|        |    | 7.1  | GATCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGGATCATCTATCCTGGTGACTCT  |
|        |    | 141  | GATACTATATACAGCCCGTCCTTCCGAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCACCCCT  |
|        |    | 211  | ACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGACAGGGTTGTAGTGG   |
|        |    | 281  | TGGTAAATGCTACGAGAAAATGTATGCTTCTGATATCTGGGGCAGGGGAACCCTGGTCACCGTCTCGAGT   |
|        |    | 351  | GGAGGCGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGAAGTGCACTTTCCTATGAGCTGACTCAGC   |
|        |    | 421  | CACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATCTTCTTGTTCTGGAAGCACGTCCAACATCGG  |
|        |    | 491  | AAGGAATTCTGTATTTTGGCACCAGCAGTTACCAGGAACGGCCCCCAAAGTCCTCATCTCTGATAAT  |
|        |    | 561  | CAGCGACCCTCAGGGGTCTCTGACAGATTCTCTGGCTCCGACTCTGGCCACCTCAGCCTCCTGGTCATCA   |
|        |    | 631  | GTCGCCTCCGGTTCGAAGATGAGGGTGATTACTACTGTGCAGCATGGGATGACAGTCTGAGTGCTTATGT   |
|        |    | 701  | CTTCGGAAGTGGGACCAAGCTGACCGTCCTAGGTGCGGCCGC   |
| scFv12 | 48 | П    | GGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAGGGTCTCCTGCAAGGCTTCTGGAGACACCTTCAGCTA   |
|        | :  | 71   | CAATGCTATCAACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGGATGGGAGGGA   |
|        |    | 141  | TTTGGTACAGCAAAGCACACAGAAGTTCCAGGGCAGAGTCACGTTTACCGCGGACGAATCCACGAGCA   |
|        |    | 211  | CAGCCTACATGGAGTTGACTAGGCTGAGATCCGAGGACACGGCCATGTATTACTGTGCGCGGGGCTC  |
|        |    | 281  | GTACAGTAATTACGAGAGGGGGTATTACTATCACATGGACGTCTGGGGCCAGGGAACCCTGGTCACCGTC   |
|        |    | 351  | rcargiggaggcggcggticaggcggaggiggciciggcgggggggggaagigcacigccigigacic   |
|        |    | 421  | AGCCACCCTCAGCGTCTGGGGCCCCCCGGGCAGGATCACCATCTCTTGTTCCGGAAGCACCTTCAACAT  |
|        |    | 491  | CGGGAGAAATTATGTTGACTGGTATAAACAACTCCCCGGAACGGCCCCTAAAACTCTTCATCATTAAGAAT  |
|        |    | 561  | GATCAGCGACCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCTGGTCG  |
|        |    | 631  | TAAGTGGACTCCGCTCCGAGGATGAGGCTGATTATTACTGTCTGACTTGGGATGACAGCCTGAGTGGTCC   |
|        |    | 701  | GGTGTTCGGCGGGGGACCAAGCTGACCGTCCTAGGTGCGGCCGC   |
| scFv13 | 49 | Н    | GCTGCAGGAGTCCGGCCCAGGACTGGTGAAGCCTTCGGGGACCCTGTCCCCTCACCTGCGCTGTCTCTGGT  |
|        |    | 71   | GGCTCCATCAACAATAATAATTGGTGGAGTTGGGTCCGCCAGCCCCCAGGGAAGGGGCTGGAGTTG   |
|        |    | 141  | GGGAAATCTATCAGAGTGGGAGCACCAACTACAACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGA   |
|        |    | 211  | CAAGTCCAACAACCAGTTCTCCCTGAAGATGAGTTCTGTGACCGCCGCGGGACACGGCCGTGTATTACTGT  |
|        |    | 281  | GCGAGGCTTAACTGGAACCACGGCCCTACTACGGTATGGACGTCTGGGGGCAGGGGCACCCTGGTCACCG   |
|        |    | 351  | TCTCGAGTGGAGGCGCCGCTTCAGGCGCGCTGGCTCTGGCGGTGGCGGAAGTGCACAGTCTGTGCTGAC  |
|        |    | 421  | GCAGCCGCCCTCAGCGTCTGGGACCCCCGGACAGAGTCACCATCTCTTGTTCTGGAAGCAGCTCCAAC   |
|        |    | 191  | ATCGGAAGTAATTTTGTATACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAACTCCTCATCTATAGGA   |
|        |    | 561  | ATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGCCTCCAAGTCTGGCACCTCAGCCTCCCTGGC   |

|        |    | 631         | CATCAGTGGGCTCCGGTCCGAGGATGAGGCTGATTATTACTGTGCGGCATGGGATGACAGGCGTGTGGTA  |
|--------|----|-------------|---|
|        |    | <b>&gt;</b> | TICGGCGGAGGGACCAAGCIGACCGICGGCCGC   |
| scFv14 | 20 |             | GGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTC  |
|        |    | 71          | TCTGGCGGCCCCGGTCGCTAGTAGTACTACTGGGGCTTCATCCGCCAGCCCCCAGGAAAAGGGCTGG   |
|        |    | 4           | AGTGGATTGGGAGTATTTATGATGGTGGCTACCACCTACAGCCCGTCCCTAAAGAGTCGAGCTACCAT  |
|        |    | 211         | ATCCTTCGACACGTCCAAGAACCAGGTCTCCCTGAACCTGACCTCTGTTACCGCCGGGGACACGGCCGTC  |
|        |    | 281         | TATTACTGTGCGAAAGACCCGGGCAGTTTGAGCGCCTTCTGGGGCCAGGGAACCCTGGTCACCGTCTCGA  |
|        |    | 351         | GIGGAGGCGCCGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGAAGTGCACTTGACATCCAGTTGACCCA   |
|        |    | 421         | GICTCCATCCTCCCTGTCTGCGTCTGTAGGAGACAGAGTCACCATCACTTGCCGGACAAGTCAGCGCATT  |
|        |    | 491         | AGCAGCTATTTAAATTGGTATCAGCAGAAGCCAGGGAAAGCCCCCTAAGCTCCTGATCTATGCTGCATCCA   |
|        |    | 561         | GITIGCAAAGIGGGGTCCCAICAAGGIICAGIGGCAGIGGTTCIGGGACAGAITICACICICACCAICAG  |
|        |    | 631         | CAGTCTGCGACCTGAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGATCACCTTCGGC  |
| scFv15 | 51 |             | CTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGAGACTCTCTGTGCAGCCTCTGGAT  |
|        | 5  | 71          | TCACCITTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGC  |
|        |    | 141         | TATTAGTGGTAGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCCGGTTCACCATCTCCAGAGAC  |
|        | •  | _           | AATICCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGGAGGACACGGCCGTGTATTACTGTG   |
|        |    | 281         | CGAGAGATTGGAGATGGCAACAATTTGGGGGCTGGTTCGACCCCTGGGGCAGAGGCACCCTGGTCACCGT  |
|        |    | S           | CTCGAGTGGAGGCGGCGGTTCAGGCGGGGGGGCTCTGGCGGTGCCGGAAGTGCACTTGATGTGTGTG   |
|        |    | 421         | ACTCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGTCACCCTCTCCTGCAGGGCCAGTCAGA  |
|        |    | σ           | GTGTTGGCAGCAAGTTGGCCTGGTACCAGCAGAAACCTGGGCAGGCTCCCAGGCTCCTCATCTTTGGTAC  |
|        |    | 9           | ATCGACCAGGGCCAGTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGGTCTGGGACAGAGTTCACTCTCACC   |
|        |    | 631         | ATCAGCAGCCIGCAGICIGAAGAITIIGCAGITIAIIACIGICAGCAGIAIAAIAACIGGCCICCGIACA  |
|        |    | $\circ$     | CTTTTGGCCAGGGGACCAAGGTGGAAATCAAACGTGCGGCCGC   |
| scFv16 | 52 | 1           | GCTGAGGTGAAGAAGCCTGGGGACTCAGTGAAGGTCTCCTGCAAGGCCTCTGGTTACAGGTTTGAAACCT  |
|        |    | _           | ATGGTTTCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGAT  |
|        |    | 4           | TGGTAAGACAAATTATGCACAGAAGTTCCAGGGCAGAGTCACCATGACCACAGACACGTCCACGAGCACA  |
|        |    | 211         | GCCTACATGGAGTTGAGGAGCCTGAGATCGGACGACGCCGTGTATTTTTTTT  |
|        |    | 281         | ATAGCAGAGGTTATTGGAACCATTACTTCTCCGACTACTGGGGGGGG   |
|        |    | S           | TGGAGGCGGCGGTTCAGGCGGAGGTGGCTGCGGGGAAGTGCACAGTCTGTGCTGACTCAGCCA   |
|        |    | 421         | CCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGAA  |
|        |    | S)          | GTAATTATGTATACTGGTACCAGCAGCTCCCAGGAACGCCCCCCAAACTCCTCATCCATAAGAATAATCG  |
|        |    | 561         | GCGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCGGCCATCAGT   |
|        |    | 631         | GGGCTCCGGTCCGAGGATGAGGCTGATTATCACTGTGCAGCGTGGGATGACAGCCTGAGTGTGTGGTTT   |
|        |    | 701         | TCGGCGGAGGGACCAAGGTCACCGTCCTAGGTGCGGCCGC  |
| scFv17 | 53 | 1<br>71     | TTGGAGTCTGGGGGGGCTTGGTACAGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCA CCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGAGCTGGAGTGGGTCTCAGCTAT |
|        |    |             |   |

|        |    | 211 | TAGTGGTAGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAAT TCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGGCCGAGGACACGGCCGTGTATTACTGTGGA GAGATTGGAGATGGAGCTGGTTCGACCCTGGGGCCTGGGGCCGAGGGACAATGGTCACCGTCTC |
|--------|----|-----|---|
|        |    | 351 | GAGTGGAGGCGGCGGTTCAGGCGGAGGTGGCTCTGGCGGGGAAGTGCACTTGAAACGACACTCACG<br>CAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGTGATAGAGCCACCCTCTCCTGCAGGGCCAGTCACAGTG  |
|        |    | 491 | TTAGTCACAACCACTTAGCCTGGTACCAGCAAAATCCTGGCCAGGCTCCCAGGCTCCTCATTTTTGGTGC ATCCAGGACAGGA  |
|        |    | 631 | ATCAGCAGACTGGAGCCTGAAGATTTTGCATCATATTACTGTCAGCAGTATGGTAGCCCCCGGCGGACGT  |
| ļ      |    | 701 | TCGCCCAAGGGACCAAGGTGGAAATCAAAGCGTGCGCCGC  |
| scrv18 | 54 | 7.1 | GAAGAAGCCTGGGTCCTCGGTGAGGGTCTCCTGCAAGGCTCGGAGGGCACCTTCGGCACTTCGGCACTTTACTACTACTACTACTACTACTACTACTACTACTA  |
|        |    | 141 | CAAACTACGCACAGAAGTTCCAGGGCAGAGTCACCATTACCGCGGACAAATCCACGACCACAGCCCACAT  |
|        | -  |     | GGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTCTATTACTGTGCGAGAGGCGGACTGGGACGATTT  |
|        |    |     | TTTGACGCCCCTCCCACTTCTCCTACTACATGGAAGTCTGGGGCAAAGGAACCCTGGTCACCGTCTCGA   |
|        |    | 351 | GTGGAGGCGCCGCTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGAAGTGCACAGTCTGTGCTGACGCAGCC  |
|        |    |     | GCCCGCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTTCTGGAAGCAACTCCAACATCGGA  |
|        |    |     | AGAAATTATGTCTACTGGTATCAGCAGCTCCCAGGAGCGGCCCCCCAAACTCCTCATCTATAGGAATAATC   |
|        |    |     | AGCGGCCCTCAGGGGICCCIGACCGAIICTCIGGCICCAAGICCGGCCCTCAGCCTCCCTGGCCAICAG   |
|        |    |     | TGGGCTCCGGTCCGAGGATGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGAGTGGCCCTGCA  |
|        |    |     | TTCGGCGGAGGGACCAAGCTGACGTCCTAGGTGCGGCCGC  |
| ScFv19 | 55 |     | AGGTCCAGCTGGTACAGTCTGGGGCTGAAGGAAGCCTGGGTCGTCGTGAAGGTCTCCTGCAAGGC   |
|        | }  | 71  | TTCTGGAGGCACCTTCAGCAGCGATGCTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGACTTGAGTGG  |
|        |    | 141 | ATGGGAAGGATCATCCCTCTAATTAATATACCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTA  |
|        |    | 211 | CCGCGGACAAATCCACGACCACAGCCTACATGGAGCTGACCAGCCTAAGATTTGAGGACGCGGCCGTGTA  |
|        |    | 281 | TTACTGTGCGAGAGTGAATAACTGGAACGCCTTTGACCAGTGGGGCCGGGGAACCCTGGTCACCGTCTCG  |
|        |    | 351 | AGIGGAGGCGCGCTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGAAGTGCACTTTCTTCTGAGCTGACTC   |
|        |    | 421 | AGGACCCTGCTGTGTCTGTGGCCTTGGGACAGACAGTCAGGATTACATGCCAAGGAGACACCCTCACAAG  |
|        |    | 491 | TTATTATGCGGCCTGGTACCAGCAGGACAGGCCCCCCCCC  |
|        |    | 561 | CGGCCCTCAGGGATCCCAGAGCGATTCTCGGCTCCAGCTCAGGAAATATTGCTTCCTTGACCATCACTG   |
|        |    | 631 | GGGCTCAGGCGGAGGATGAGGGTGACTTTTACTGTAGTTCCCGGGACAGCAGTGGGTACCGTTTTGTCTT  |
|        |    | 701 | CGGGGCTGGGACCAAGCTGACGTCCTAGGTGCGGCCGC  |
| scFv20 | 56 |     | GAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCTGGAGGCACCTTCACCAGCTATGCAATC  |
|        |    | 71  | AGTIGGGIGCGACAGGCCCCTGGACAAGGGCTIGAGIGGAIGGGAGGGTICAICCCTGIAITIGGCACAG  |
|        |    | 141 | CAAACTACGCACAGAAGTIGCAGGGCAGAGTCACGATCACCGCGGACGATICCATGACCACGGGTGTACAT   |
|        |    | 211 | GGAGCTGAGTAGCCTGACCTCTGAAGACACGGGCGTGTATTACTGTGCGAGAGATCTCATGCGGCTGGCC  |
|        |    | 281 | CGTCGCGATGAATACTACTATTACTACATGGACGTCTGGGGCCCAAGGGACAATGGTCACCGTCTCGAGTG   |

|        |    | 351 | CAGGCCGCTTCAGGCGGAAGCTGGAAGCTTGGCGGAAGCTGGAAGCTGGAAGTGCAAGTAGAAGTTGAAGTTGAAGAAGAAGAAGAAGAAGAAGA |
|--------|----|-----|---|
|        |    | 421 | CGCAGCGTCTGGGACCTACGGGCAGAAGATCACCATCTCTTGTTCTGGAAGCAGTTCCGAATATCGGAGTT                         |
|        |    | 491 | AATTATGTTTACTGGTACCGGCAATTCCCAGGAGCGGCCCCCCCC   |
|        |    | 561 | GGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCCGCCTTCGGCCATCAGTGG                            |
|        |    | 631 | GCTCCGGTCCGAGGATGAGGCTGATTATTATTGTTCCACATGGGATGACACCCTGAGTGGTTATATCTTC                          |
|        |    | 701 | GGAGTTGGGACCAAGGTCACCGTCCTAGGTGCGGCCGC  |
| scFv21 | 57 | 1   | CAGCCTGGGGGGTCCCTGAGACTCTCCTGTGGATTCACCTTTAGCAGCTATGCCATGAGCT                                   |
|        |    | 71  | GGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTGGTGGTAGCACATA                             |
|        |    | 141 | CTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCAGAGACAATTCCAAGAACACGCTGTATCTGCAA                         |
|        |    | 211 | ATGAACAGCCTGAGAGCCGGAGGACACGGCCGTGTATTACTGTGCGAGAGATTGGAGATGGCAACAATTTG                         |
|        |    | 281 | GGGGCTGGTTCGACCCCTGGGGCCAGGGCACCCTGGTCACCGTCTCGAGTGGAGGCGGCGGCGGTTCAGGCGG                       |
|        |    | 351 | AGGTGGCTCTGGCGGTGGCGGAAGTGCACTTTCTTGAGCTGACTCAGGACCCTGCTGTGTCTGTGGCC                            |
|        |    | 421 | TIGGGACAGACAGTCAGGATCACGATGCCAAGGAGACAACCTCAGAAGTTTTTCTGCAAGCTGGTACCAGC                         |
|        |    | 491 | TGAAGCCAGGACAGGCCCCTGTACTTGTCATGGTAAGAACAACCGGCCCTCAGGGATCCCAGACCG                              |
|        |    | 561 | ATTCTCTCCCCCCCCAGCTCAGGAAACACAGCTTCCTTGGCCATCACTGGGGCCTCTGGCGGAAGATGAGGCT                       |
|        |    | 631 | GACTACTACTGTAACTCCCGGGACAGCAGTGGTAACCCTTATGTCTTCGGAACTGGGACCAAGGTCACCG                          |
|        | ′  | 701 | TCCTAGGTGCGGCCGC  |
| scFv22 | 58 |     |   |
|        |    |     | GGTCTTCGGTGAAGGTCTCCTGCAAAATTTCCGGAGGCAATCTCAATAGGCTTACTGTCACTGGGGGGGG                          |
|        |    | 71  | ACAGGCCCCTGGACAAGGCCTTGAGTGGGTGGGCAGGATTCTTCCCGACTCAGTAAATCAAGTCGTGAAG                          |
|        |    | 141 | TICCAGCGCAGACTCAAACTGACCTCTGACACTTCCACGCGCACAGCCTATTTAGAACTGAGGAGCCTGA                          |
|        |    | 211 | AATCTGAAGACACGCCGTCTATTATTGTGCGGCGTCATCTAAAATAGGCTTCCAGGTTGGGGAGCTCGA                           |
|        |    | 281 | CTACTGGGGCCGGGCACCCTGGTCACCGTCTCGAGTGGAGGCGGCGGTTCAGGCGGGGGGGG                                  |
|        |    | 351 | GGTGGCGGAAGTGCACAGTCTGTCGTGACGCAGCCGCCCTCAGCGTCTGCTACCCCCGGGCAGAGGGTCA                          |
|        |    | 421 | CCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGAAGAAATTATGTCTACTGGTACCAGCAGGTCCCAGG                          |
|        |    | 491 | AACGGCCCCCCAACTCCTCGTCTATAACAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGC                          |
|        |    | 561 | TCCAAGTCTGGCACCTCAGCCTCCCTGGGCATCAGTGGGCTCCGGTCCGAGGATGAGGCTGATTATTACT                          |
|        |    | 631 | GTTCAACATGGGATGACAGCCTGAGTAGTCCGGTATTCGGCGGGGGGGG   |
|        |    | 701 | COCCCC  |
| scFv23 | 29 |     | CACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGGCTGGAGTGGGTCTCAGCT                         |
|        |    | 71  | ATTAGTGGTAGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACA                             |
|        |    | 141 | ATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGGAGGACACGGCCGTGTATTACTGTGC                         |
|        |    | 211 | GAGAGGTAGACGCCGCGAGAGCATATTAATATGATTCGGGGAGTTAGACCACAATACGACGACTCTGGC                           |
|        |    | 281 | ATGGACGTCTGGGGCCGGGCACCCTGGTCACCGTCTCGAGTGGAGGCGGCGGTTCAGGCGGGGGGGCTTCAGGCGGGGGGGG              |
|        |    | 351 | CTGGCGGTGGCGGAAGTGCACTTTCCTATGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCA                          |
|        |    | 421 | TAGGGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGAAGTAATTATGTATACTGGTACCAGCAG                          |
|        |    | 491 | CTCCCAGGAACGCCCCCCAAACTCCTCATCTATAGGAATAATCAGCGGCCCTCAGGGGTCCCTGACCGAT                          |

|        |          | 17.0 | THE CHARLES AND A CARREST OF A |
|--------|----------|------|---|
|        |          | 707  | ICICITEGECICCEMETICION CONTRA |
|        |          | 701  | CTAGGTGCGCCGC   |
| scFv24 | 09       | н    | GCTATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAG  |
|        |          | 71   | TGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAAC  |
|        |          | 141  | ACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAAATACAG  |
|        |          | 211  | GAAAGGGCATTACTTTGGTTCGGGGAGTATTGTCAGGACTGTGACCGCAGTTCTACATCCCGCATGGA  |
|        |          | 281  | CGTCTGGGGCCAGGGCACCCTGGTCACCGTCTCGAGTGGAGGCGGCGGTTCAGGCGGAGGTGGCTCTGGC  |
|        |          | 351  | GGTGGCGGAAGTGCACAGGCTGTGCTGACTCAGCGTCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCA   |
|        |          | 421  | CCATCTCTTGTTCTGGAAGCACCTCCAACATCGGAAGGAA  |
|        |          | 491  | AACGGCCCCCAAACTCCTCATCTATAGGAATAATAAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGC  |
|        |          | 261  | TCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGGTCCGAGGATGAGGCTGATTATTACT  |
|        |          | 631  | GTGCAGCTTGGGATGACAGCCTGAGTGGTTGGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTGC<br>GGCCGC  |
| scFv25 | 61       |      | AGGCTTGGTACAGCCTGGGGGGTCCCCGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGCAGCTAT  |
|        | <b>.</b> | 71   | GCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTTGGAGTGGGTCTCAGCTAATTAGTGGTAGTTGTG  |
|        |          | 141  | GTAGCACATACTACGCAGACTCCGTGAAGGCCCGGTTCACCATCTCCAGAGACATTCCAAGAACACGCT   |
|        |          | 211  | GTATCTGCAAATGAACAGCCTGAGAGCCGGAGGACACGGCCGTGTATTACTGTGCAAAAGATATGGGGATAC  |
|        |          | 281  | AGTTATGGTTACGGGACGAGGGGCCTCTTTGACTACTGGGGCCGAGGGACAATGGTCACCGTCTCGAGTG  |
|        |          | 351  | GAGGCGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGAAGTGCACAGTCTGTCGTGACGCAGCCGCC  |
|        |          | 421  | CTCAGCGTCTGGGGCCCCCGGGCAGGATCACCATCTTCTTGTTCCGGAAGCACCTTCAACATCGGGAGA   |
|        |          | 491  | AATTATGTTGACTGGTATAAACAACTCCCCGGAACGGCCCCCAAACTCTTCATCTATAAGAATGATCAGC  |
|        |          | 561  | GACCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGTCGTAAGTGG  |
|        |          | 631  | ACTCCGCTCCGAGGATGAGGCTGATTATTACTGTCTGACTTGGGATGACAGCCTGAGTGGTCGGTGTTC   |
|        |          | 10/  | GGCGGGGGGCCAAGGTCACCGTCCTAGGTGCGGCCGC   |
| scFv26 | 62       | -1   | TGGAGTCTGGGGGGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCAC  |
|        |          | 7.1  | CITIAGCAGCIATGCCCATGAGCTGGGTCCGCCAGGCTCCACGGAAGGGGCTGGAGTGGGTCTCAGCTATT   |
|        |          | 141  | AGTGGTAGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATT   |
|        |          | 211  | CCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCCGAGGACACGGCCGTGTATTACTGTGCGAG   |
|        |          | 281  | AGATIGGAGAIGGCAACAATIIGGGGGCTGCTICGACCCCTGGGGGGGGGG   |
|        |          | 351  | AGTGGAGGCGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGAAGTGCACTTGAAACGACACTCACGC  |
|        |          | 421  | AGICICCAGCCACCTGICIGICITCTCCGGGGGACAGAGCCACCCTCTCCTGCAGGGCCCAGTCAAAGTAI   |
|        |          | 491  | TGGTGGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAGCCTCCCAGGCTCCTCATCTTTGGTGCATCC  |
|        |          | 561  | ACTAGGGCCTCTGGTACCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCA  |

|          |    | 631 | GCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTATAATAACTGGCCTCCATGGACTTT              |
|----------|----|-----|---|
| cc.Fv.77 | 63 |     | ならなるというというというというというというというというというというというというというと  |
| 2CF V2./ | 60 | - : | ACASCAL SESSES COLL GAGACIO L'EL GOACCIO L'ESCAL TOCCITTAGCAGCIATGAGC               |
|          |    | 7   | TGGTCCGCCAGGCTCCAGGGAAGGGGCTGCAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGTAGTAGTAGTAGTAGTAGT |
|          |    | 141 | ACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCA              |
|          |    | 211 | AATGAACAGCCTGAGAGGACACGGCCGTGTATTACTGTGCGAAAGGGGGACGGGGTAGTGGCTGGA                  |
|          |    | 281 | ACTACGTACTACTACGGTATGGACGTCTGGGGGCGGGGGACCACGGTCACCGTCTCGAGTGGAGGGC                 |
| ,        |    | 351 | GCGCTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGAAGTGCACAGTCTGTGCTGACGCAGCCGCCCTCAGC              |
|          |    | 421 | GTCTGGGGCCCCCGGGCAGGATCACCATCTTTGTTCCGGAAGCACCTTCAACATCGGGAGAAATTAT                 |
|          |    | 491 | GTTGACTGGTATAAACAACTCCCCGGAACGGCCCCCAAACTCTTCATCTATAAGAATGATCAGCGACCCT              |
|          |    | 561 | CAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGTCGTAAGTGGACTCCG              |
|          | _  | 631 | CTCCGAGGATGAGGCTGATTATTACTGTCTGACTTGGGATGACAGCCTGAGTGGTCCGGTGTTCGGCGGG              |
|          |    | 701 | GGGACCAAGCTGACCGTCCTAGGTGCGGCCGC  |
| scFv28   | 64 | ٢   | GGCCTCTGGATTCGGCCTCAATGGCTATGAAATGCATTGGGTGCGCCCAGGCCCCGGACAAAGGCTTGAG              |
|          | _  | 71  | TGGCTGGCCCGGATCAACGCTGCCATTGGCGACACACGGTATTCAAGGGGAGTTCCAGGATAGAGTCTCCA             |
|          |    | 141 | TTACCAGAGACATGTCCGCGAACACAGTCTACATGGAGATGAGCAGGCTGAGATTTGAAGACACGGCTGT              |
|          |    | 211 | TTATTATTGTGTGAGATTCCACGATTGGCGACATTGTAATAGTGCCCACCTGTCAGCCCCCTTTTGACCAC             |
|          |    | 281 | TGGGGCAAGGGAACCCTGGTCACCGTCTCGAGTGGAGGCGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTG              |
|          |    | 351 | GCGGAAGTGCACTITCITCIGAGCTGACTCAGGACCCTGCTGTGTCTCTGGGCCTTGGGACAGACA                  |
|          |    | 421 | GATCACATGCCAAGGAGACAGCCTCAGATACTATTCTGCAAGTTGGTACCGGCAGAAGCCAGGGGAGGCC              |
|          |    | 491 | CCTGTTATTGTCATGTATGGTAACACCCGCCGGCCCTCAGGGATCCCCAGACCGAATCTCTGGCTCCAGCT             |
|          |    | 561 | CAGGAAACACAGCTTCCTTGACCATCAGTGGGGGTCAGGCGGAAGATGAGGCTGACTATTATTGTAACTC              |
|          |    | 631 | CCGAGACAGTAGTGGTAACCATCTGGTCTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTGCGGCGC                |
| scFv29   | 65 | 1   | GTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCTCTGGATTCACCTTTAGCAGCTATGCCATGA               |
|          |    | 71  | GCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGCAGCAC              |
|          |    | 141 | ATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTG              |
|          |    | 211 | CAAATGAACAGCCTGAGAGCCGGGGACACGGCCGTGTATTACTGTGCGAGAGATCATCGGTCGG                    |
|          |    | 281 | GAGGTGGGAGCTACTTACTACGCCCTTTGGACTACTGGGGCCAAGGGACAATGGTCACCGTCTCGAGTGG              |
|          |    | 351 | AGGCGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGAAGTGCACTGCCTGTGCTGACTCAGCCACCC               |
|          |    | 421 | TCAGCGTCTGGGACCCCCGGGCAGAGGTCACCATCTTGTTCTGGAAGCAGCTCCAACATCGGAAGGA                 |
|          |    | 491 | ATTATGTATACTGGTACCAGCAGCTCCCCAGGAACGGCCCCCAAACTACTACTAGAATAATCTGCG                  |
|          |    | 561 | GCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGG              |
|          |    | 631 | CTCCGGTCCGAGGATGAGGCTGATTATTACTGTGCAGCATGGGATGACACCCTGAGTGGTGGTATTCG                |
|          |    | 701 | GCGGAGGGACAAAGCTGACGTCCTAGGTGCGGCCGC  |
| scFv30   | 99 | ~   | CGGAGGTGAGGAAGCCTGGGGCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGATTCACGTTCACTAGTTA              |
|          |    | 7.1 | TCTATTCCATTGGGTGCGCCCAGGCCCCCGGACAAAGGCTTGAGTGGATGGGGGTGGATCAACGCTGGCAAT            |
|          |    | 141 | GGAAACACAAAATATTCACCGAAGTTCCAGGGCAGAGTTACCCTTACCGGGGACACATCCACGAGCACAA              |

4.6.4

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|        |    | 211 281 351 | CCTACATGGAGCTGAGCAGCCTGACATCTGAGGACACGGCTGTTTATTACTGTGCGAGAGATCAGGTGTT CTATGAGAGTGGTTCTTACTACATACGCCCTTCTTTTGACTTCTGGGGCAGGGCACCCTGGTCACCGTC   |
|--------|----|-------------|--|
|        |    | 421         | TOTICARSTRANGEGESTICAGEGEGEGEGEGEGEGEGEGEGEGEGEGEGEGEGEGEGE  |
|        |    | 561         | TTAGCCAGGCCCCCATCAAGGTTCAGCGCGCAGTGGGATCTGGGACAGATTTCACTCTCACCATCAGCA  |
|        |    | 631         | GCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAATATAGTAATTATCCGCTCACTTTCGGCGG<br>AGGGACCAAGCTGGAGATCAAACGTGCGGCCGC  |
| scFv31 | 19 | 1           | TGGTACGGCCTGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGGCAT  |
|        |    | 71          | GAGCTGGGTCCGCCAAGCTCCAGGGAAGGGGCTGGAGTGGGTCTCTGGTATTAATTGGAATGGTAGCTAGC  |
|        |    | 141         | ACAGGTTATGCAGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCCTGTATC<br>TGCAAATAAACAGTCTGAGAGCCGAGACACAGACAACAAATTAAAAAAAA   |
|        |    | 281         | TATTGGGGCAGAGGGAATGGTCACCGTCTCGAGTGGAGGCGCGGTTCAGGCGAGGCGAGGTCGC   |
|        |    | 351         | GGTGGCGGAAGTGCACTTTCTTCTGAGCTGACTCAGGACCCTGCTACTGTGTCTGTGGCCTTGGGACAGA   |
|        |    | 421         | CAGTCAGGATAACTTGTCAGGGCGACAGCCTCGACAAATATTATGCAACCTGGTATCAACAGAAGCCTGG   |
|        |    | 4 y L       | ACAGECCCCTCTACTTGTCTTCTTCTTTTTTTTTTTTTTT   |
|        |    | 631         | ICCARCICCGGGAAATCGGTACTAATCGAATCCTATTCGGCGGAGGGACCAAGCTGACGTGCTGCTATTACT   |
|        |    | 701         | 292299   |
| scFv32 | 89 |             | TTGGTTCAGCCTGGAGGGTCCCTGAGACTCTCCTGTGCAGCCGCTGGATTCACCTTCAGTACTTTTGAAA   |
|        |    | 71          | TGAATTGGGTCCGCCCAGGCCCCCAGGGAAGGGCCTGGAGTGGGTTTCATATTAGTGGTAGTGGTCATGC   |
|        |    | 711         | CHIGIAD ATGABORGOOD BOOCO ACCOUNTION CONTRACTOR AND ACCOUNTS AND ACCOU |
|        |    | 281         | くこくなどとなっていまっていることになっていることでは、「できまれている」、「おう」、「おう」をいることはなられる方面をおからしている。 でき できまり できまり かいしゅうしゅう しゅうしゅうしゅう しゅうしゅうしゅう しゅうしゅうしゅう しゅうしゅうしゅう しゅうしゅうしゅう しゅうしゅうしゅう しゅうしゅうしゅう しゅうしゅう しゅう  |
|        |    | 351         | TACTITACCANCIACOGACTICOGALAIGGACGICIGGGGGGGGGGGGGGGGCACCACGGICACCGICICGAGIGGAGG<br>CGGCGGTTCAGGCGGAGGTGGCTCTGGCGGGAGGGGGAGTGCACTGTGCTGACTCAGCTAACTCACTC  |
|        |    | 421         | GCGTCTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTTCTGGAAGCAGCACCAACAACGAGTAATA   |
|        |    | 491         | CITTAAACTGGTACCAGCAGCTCCCAGGAACGCCCCCCAAACTCCTCATCTATAGTAATGATCAGCGGCC   |
|        |    | 561         | CTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTC   |
|        |    | 631         | CAGTCTGAGGATGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGAATGGCTGGTGTTCGGCG  |
|        |    | 701         | GAGGGACCAAGGTCACCGTCCTAGGTGCGCCCGC   |
| scFv33 | 69 |             | AGGGCCTCTGGGGGGACCTCCAGCAGTTCTGCTTTCAGCTGGGTGCGACAGGCCCCTGGACAGGGGCTTC   |
|        |    | 77          | AGTGGATGGGAGGGATCATCCCTCTTTTGGTGCAGCAAACTACGCACAAAAGGTCCGGGCCGGACTCAC  |
|        |    | 141         | GATTACCGCGGACGACGACGCCACGTCTTACATGAAACTGGAAAATTTGCAGTCTGACGACACGGCC  |
|        |    | 211         | GTTTATTTCTGTGCGACTAACGGACAGACGAGGTCGCCACCCGGCTACTACTACGCATGGACGTCTGGG  |

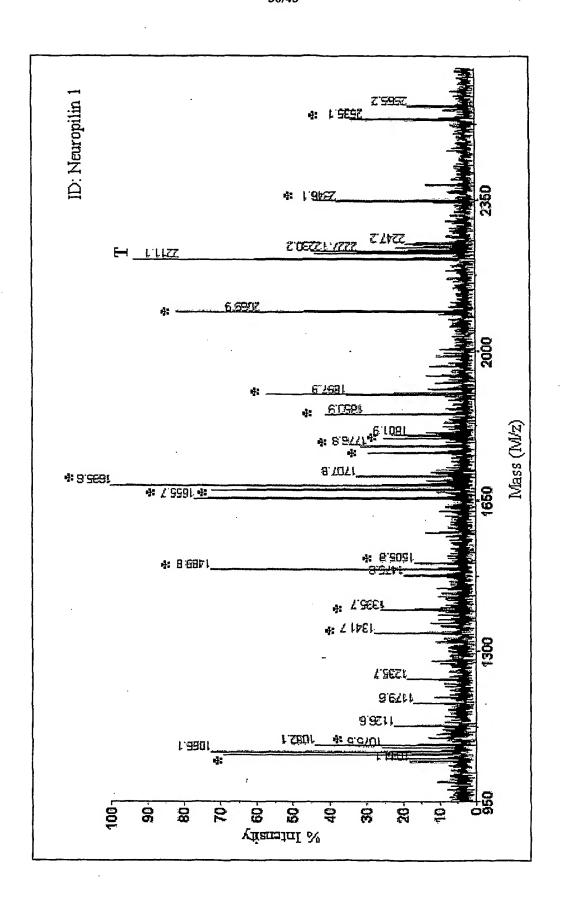
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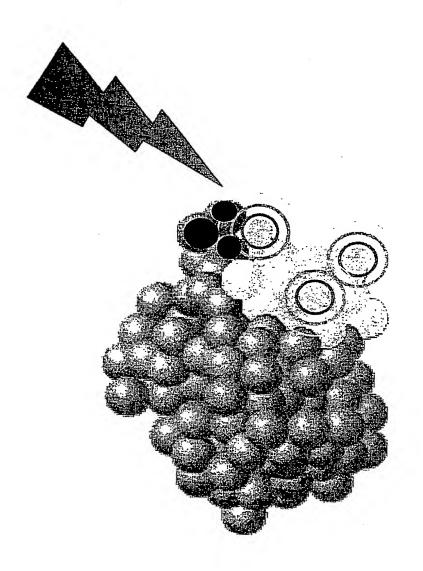
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|--------|----|-------|---|
|        |    | 187   | GCCGAGGCACCCTGGTCACCGTCTCGAGTGGAGGCGGCTTCAGGCGGAGGTGGCTCTGGCGGTGGCGG      |
|        |    | 351   | AAGTGCACAGTCTGTGTTGACGCAGCTGCCCTCAGCGTCTGGGGCCCCCGGGCAGGATCACCATCTCT      |
|        |    | 421   | TGTTCCGGAAGCACCTTCAACATCGGGAGAAATTATGTTGACTGGTATAAACAACTCCCCGGGAACGGCCC   |
|        |    | 491   | CCAAACTCTTCATCTATAAGAATGATCAGGGACCCTCAGGGGTCCCTGGCCGATTCTCTGGCTCCAAGTC    |
|        |    | 561   | TGGCACCTCAGCCTCCCTGGTCGTAAGTGGACTCCGCTCCGAGGATGAGGCTGATTATTACTGTCTGACT    |
|        |    | 631   | TGGGATGACAGCCTGAGTGGTCCGGTGTTCGGCGGGGGACCAAGCTGACCGTCCTAGGTGCGGCCGC       |
| scFv34 | 20 | _     | GCCTGCAAGGGTTTTGGTTACACCTTCGTCGATCATGGAATTAGTTGGGTGCGACAGGCCCCTGGACAAG    |
|        | -  | 7.1   | GGCTTGAGTGGATGGATCAACACTCACGACGGTCACAAACTATGCACAAAAAAAGACAAGGCCAG         |
|        |    | 141   | ACTCACCATGACCACAGATGCCTCCATTAATACTTCCTACATGGAGCTGCGGAGCCTGACATCTGACGAC    |
|        |    | 211   | ACGGCCGTCTATTATTGTGCCCCGGGGGGGGAGAGACTCGGACCGCACATAGATCTCGCAGGGCCACGAACG  |
|        |    | 281   | ACAATGGATATCCCTATTACTCCTCTGGTCTGGACGTCTGGGGCCCAAGGAACCCTGGTCACCGTCTCGAG   |
|        |    | 351   | TGGAGGCGCCGCTTCAGGCGGAGGTGGCTGCCGGTGGCGGAAGTGCACAGGCTGTGCTGACTCAGCCG      |
|        |    | 421   | TCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGAA    |
|        |    | 491   | GTAATTATGTATACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAACTCCTCATCTATAGGAATAATCA    |
|        |    | 561   | GCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGT    |
|        |    | 631   | GGGCTCCGGTCCGAGGATGAGGCTGATTATTACTGTGCATGAGGATGACAGCCTGAGTGGTTGGGTGT      |
|        | ,  | 701   | TCGCCGAGGGACCAAGCTGACCTCCTAGGTGCGGCCGC                                    |
| scFv35 | 71 |       | AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTACTATATGCACTG    |
|        |    | 11    | GGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGGAATAATCAACCCTAGTGGTGGTAGCACAAAGC       |
|        |    | 141   | TACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGC    |
|        |    | 211   | TGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGTTCGGGCGCCCAGAATGGTTCG   |
|        |    | 281   | GGGACITALTATAGACCCCTACGGTATGGACGTCTGGGGCCCGAGGCACCCTGGTCACCGTCTCGAGTGGA   |
|        |    | 351   | GCCGCCGCTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGAAGTGCACAGTCTGTGCTGACTCAGCCACCCT    |
|        |    | 421   | CAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATCTTTTTTTT                               |
|        |    | 491   | TTATGTATCCTGGTATCAGCAGTTCCCAGGAACGCCCCCCAAACTCCTCATCTATAGGAATAATCAGCGG    |
|        |    | 561   | CCCTCAGGGGTCCCTGACCGGTTCTCTGGCTCCAAGTCTGGCATTTCAGCCTCCCTGGCCATCAGTGGGC    |
|        |    | . 631 | TCCGGTCCGAGGATGAGGCTGATTTTTACTGTGTAGCATGACAGCCTGAGGGAATATGTCTTCGG         |
|        |    | 701   | AACTGGGACCAAGGTCACCGTCCTAGGTGCGGCCGC                                      |
| scFv36 | 72 | -     | GGAGTCTGGGGGGGCTTGGTACAGCCTGGGGGTCCCTGAGACTCCTGTGCAGCCTCTGGATTCACC        |
|        |    | 7.3   | TTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGGCTGGAGTGGGTCTCAGCTATTA   |
|        |    | 141   | GTGGTAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTC    |
|        |    | 211   | CAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGGCCGAGGACACGGCCGTGTATTACTGTGCGAAA   |
|        |    | 281   | GGTGGGACTAGGGTGACCCACCGGGGTGGTTTTGATATATGGGGCCGAGGGACAATGGTCACCGTCTCGA    |
|        |    | 351   | GTGGAGGCGGCGGTTCAGGCGGAGGTGGCTCTGGCCGTGGCGGAAGTGCACTGCCTGTGCTGACTCAGCC    |
|        |    | 421   | CCCCTCAGCGTCTGGGGCCCCCCGGGCAGGATCACCATCTCTTGTTCCGGAAGCACCTTCAACATCGGG     |
|        |    | 491   | AGAAATTATGTTGACTGGTATAAACAACTCCCCGGAACGGCCCCCAAACTCTTCATCATCTATAAGAATGATC |
|        |    | 561   | AGCGACCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCTGGTCGTAAG     |

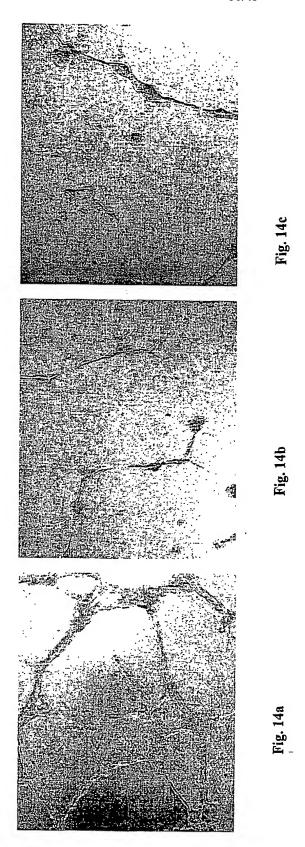
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TGGACTCCGCTCCGAGGATGAGGCTGATTATTACTGTCTGACTTGGGATGACAGCCTGAGTGGTCCGGTG 631



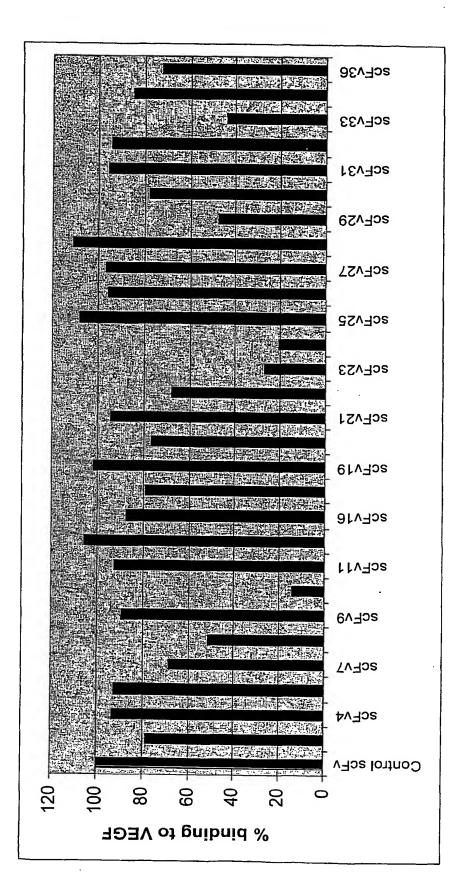






Tab. 1: Inhibition of tube formation

| scFv                  | Average inhibitory effect |
|-----------------------|---------------------------|
| control (10% PBS)     | 0.8                       |
| scFv4                 | 1.7                       |
| scFv5                 | 1.6                       |
| scFv7                 | 2.4                       |
| scFv8                 | 2.4                       |
| scFv9                 | 1.5                       |
| scFvll                | 2.2                       |
| scFv12                | 1.9                       |
| scFv13                | 2.1                       |
| scFv15                | 1.9                       |
| scFv16                | 1.6                       |
| scFv18                | 2.0                       |
| scFv19                | 1.6                       |
| scFv20                | 1.3                       |
| scFv21                | 2.0                       |
| scFv22                | 1.5                       |
| scFv23                | 2.1                       |
| scFv24                | 1.7                       |
| scFv25                | 2.3                       |
| scFv26                | 2.1                       |
| scFv27                | 2.3                       |
| scFv28                | 2.2                       |
| scFv29                | 2.1                       |
| scFv30                | 1.8                       |
| scFv31                | 2.4                       |
| scFv32                | 1.7                       |
| scFv33                | 2.1                       |
| scFv34                | 1.5                       |
| scFv35                | 1.4                       |
| scFv36                | 1.9                       |
| scFv7*                | 2.3                       |
| scFv8*                | 2.5                       |
| scFv13*               | 2.5                       |
| scFv25*               | 2.6                       |
| scFv26*               | 2.4                       |
| scFv28*               | 2.1                       |
| scFv31*               | 2.3                       |
| scFv33*               | 2.1                       |
| anti-alpha-2-integrin | 2.3                       |
| anti-NP-1             | 1.1                       |



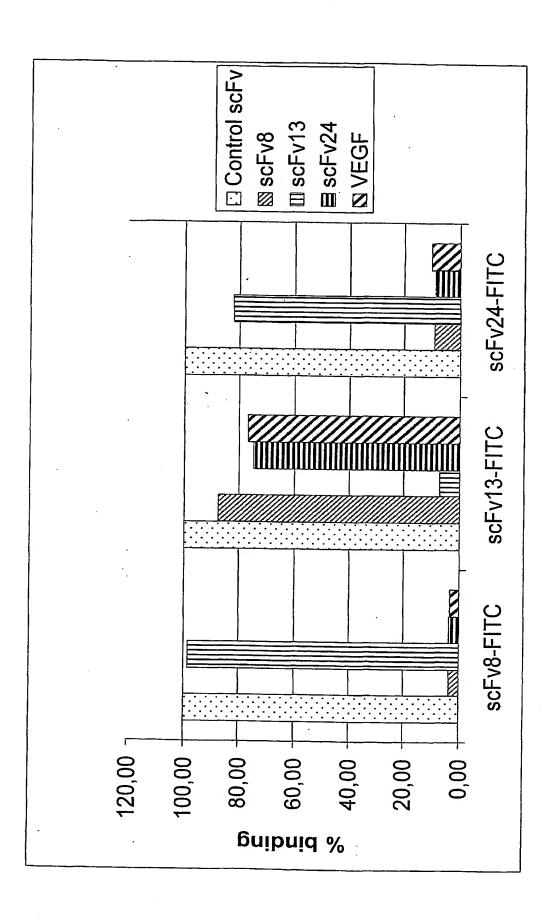


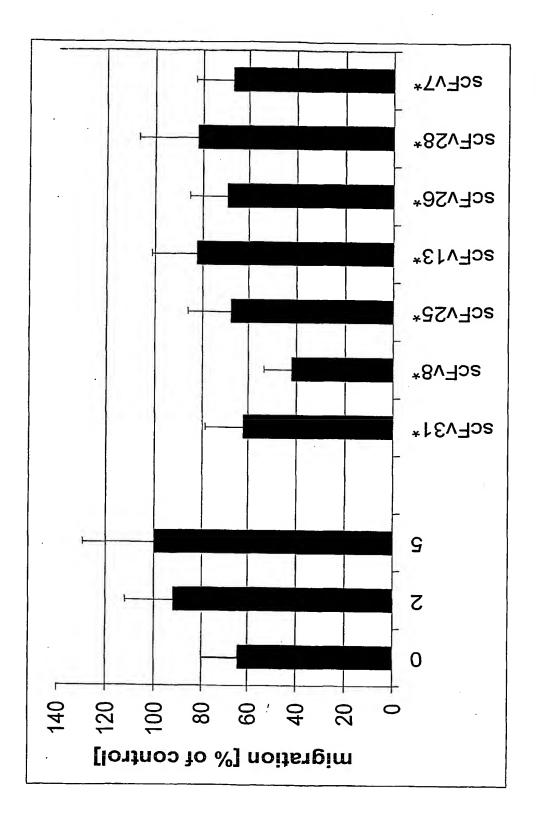
Fig. 17

## Tab.2 Transendothelial Invasion assay

| scFv   | Inhibition of Invasion |
|--------|------------------------|
| scFv26 | +                      |
| scFv27 | +                      |
| scFv34 | +                      |
| ScFv35 | +                      |

Fig. 18

PCT/EP2003/014756



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